

SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e-8.rni.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
---------------------------------	---	---------------------------------------	---------------------------	--

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-8.rni.

[start](#)

[Go Back to previous p](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 10:12:34 ; Search time 930 Seconds
(without alignments)
11415.776 Million cell updates/sec

Title: US-08-819-669E-8
Perfect score: 5674
Sequence: 1 CCCGGGGCACCACCTGGCATC.....TAATGATCTGGGTGGATCC 5674

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5674	100.0	5674	2	US-07-807-043B-8	Sequence 8, Appli
2	5674	100.0	5674	2	US-08-190-411A-1	Sequence 1, Appli
3	5674	100.0	5674	2	US-08-299-849B-8	Sequence 8, Appli
4	5674	100.0	5674	2	US-08-560-024-1	Sequence 1, Appli
5	5674	100.0	5674	2	US-08-142-368A-8	Sequence 8, Appli
6	5674	100.0	5674	3	US-08-967-727-8	Sequence 8, Appli
7	5674	100.0	5674	3	US-08-037-230D-8	Sequence 8, Appli
8	5674	100.0	5674	3	US-09-583-850-8	Sequence 8, Appli
9	5674	100.0	5674	3	US-09-579-197-8	Sequence 8, Appli
10	5674	100.0	5674	3	US-09-404-026-8	Sequence 8, Appli
11	5674	100.0	5674	3	US-09-312-464-8	Sequence 8, Appli
12	5674	100.0	5674	3	US-09-583-848A-8	Sequence 8, Appli
13	3934.8	69.3	5699	3	US-09-949-016-12445	Sequence 12445, A
14	3934.8	69.3	5699	3	US-09-949-016-14430	Sequence 14430, A
15	2655	46.8	11495	3	US-09-056-105-9	Sequence 9, Appli
16	2513.6	44.3	4895	3	US-09-056-105-10	Sequence 10, Appl
17	2429.6	42.8	4736	3	US-09-056-105-12	Sequence 12, Appl
18	2422.8	42.7	4741	3	US-09-056-105-11	Sequence 11, Appl
19	2419	42.6	2419	2	US-07-807-043B-7	Sequence 7, Appli
20	2419	42.6	2419	2	US-08-299-849B-7	Sequence 7, Appli
21	2419	42.6	2419	2	US-08-142-368A-7	Sequence 7, Appli
22	2419	42.6	2419	3	US-08-967-727-7	Sequence 7, Appli
23	2419	42.6	2419	3	US-08-037-230D-7	Sequence 7, Appli
24	2419	42.6	2419	3	US-09-583-850-7	Sequence 7, Appli
25	2419	42.6	2419	3	US-09-579-197-7	Sequence 7, Appli
26	2419	42.6	2419	3	US-09-404-026-7	Sequence 7, Appli
27	2419	42.6	2419	3	US-09-312-464-7	Sequence 7, Appli
28	2419	42.6	2419	3	US-09-583-848A-7	Sequence 7, Appli
29	2408	42.4	2420	2	US-08-465-167A-23	Sequence 23, Appl
30	2408	42.4	2420	3	US-09-056-105-4	Sequence 4, Appli
31	2408	42.4	2420	3	US-08-627-820-23	Sequence 23, Appl
32	2117.8	37.3	4559	3	US-09-056-105-5	Sequence 5, Appli
33	2058.8	36.3	4157	2	US-07-807-043B-9	Sequence 9, Appli
34	2058.8	36.3	4157	2	US-08-299-849B-9	Sequence 9, Appli
35	2058.8	36.3	4157	2	US-08-142-368A-9	Sequence 9, Appli
36	2058.8	36.3	4157	3	US-08-967-727-9	Sequence 9, Appli
37	2058.8	36.3	4157	3	US-08-037-230D-9	Sequence 9, Appli
38	2058.8	36.3	4157	3	US-09-583-850-9	Sequence 9, Appli
39	2058.8	36.3	4157	3	US-09-579-197-9	Sequence 9, Appli
40	2058.8	36.3	4157	3	US-09-404-026-9	Sequence 9, Appli
41	2058.8	36.3	4157	3	US-09-312-464-9	Sequence 9, Appli
42	2058.8	36.3	4157	3	US-09-583-848A-9	Sequence 9, Appli
43	1945	34.3	4523	3	US-09-692-401-1	Sequence 1, Appli
44	1762.6	31.1	4204	2	US-08-928-615-1	Sequence 1, Appli
45	1762.6	31.1	4204	3	US-09-056-105-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-07-807-043B-8

; Sequence 8, Application US/07807043B

; Patent No. 5342774

; GENERAL INFORMATION:

; APPLICANT: Boon, Thierry, Van den Eynde, Beno t

; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor

```

; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,043B
; FILING DATE: 19911212
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5342774man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 253.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: singular
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-07-807-043B-8

```

```

Query Match          100.0%;  Score 5674;  DB 2;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy      61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy      121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy      181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

```

Db	181		TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241		CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241		CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301		AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301		AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361		TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361		TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421		CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421		CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601		CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601		CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661		CACCCCCACCCCCACCCCCACGCCCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661		CACCCCCACCCCCACCCCCACGCCCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781		GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781		GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901		GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901		GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961		CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961		CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140

Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCC TGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Db	1621	CCAGCCC TGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040

Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041		2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101		2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161		2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221		2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281		2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341		2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401		2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461		2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521		2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581		2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Db	2641		2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701		2760
Qy	2761	CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761		2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821		2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Db	2881		2940

Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAATCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAATCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCACACTCCTGCCTGCTGCCCTGACGAGATCATCATGTCTCTTGAGCAGAGGAG	3900

Db	3841	 CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCAC TGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960
Db	3901	 TCTGCAC TGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	 TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCAC TCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	 CATCAACTTCAC TCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTG TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	 GCCAAGCACCTCTTG TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Db	4261	 AATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTG CAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	 CTCTGAGTCCTTG CAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	 CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCC TATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	 GGAGCACAGTGCC TATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800

Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACCTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACCTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640
Qy	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674
Db	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674

RESULT 2
 US-08-190-411A-1
 ; Sequence 1, Application US/08190411A
 ; Patent No. 5541104
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;
 ; APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;
 ; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;
 ; APPLICANT: Old, Lloyd J.
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO
 ; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1
 ; TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felte & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/190,411A
 ; FILING DATE: 01-FEBRUARY-1994
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 037,230
 ; FILING DATE: 26-MARCH-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/04354
 ; FILING DATE: 22-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/807,043
 ; FILING DATE: 12-DECEMBER-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/764,364
 ; FILING DATE: 23-SEPTEMBER-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/728,838
 ; APPLICATION NUMBER: 9-JULY-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/705,702
 ; FILING DATE: 23-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hanson, No. 5541104man D.
 ; REGISTRATION NUMBER: 30,946
 ; REFERENCE/DOCKET NUMBER: LUD 5354
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5674 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-190-411A-1

Query Match 100.0%; Score 5674; DB 2; Length 5674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db     61 ATCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
        |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
        |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
        |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
        |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
        |||
Db    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Qy    601 CCCCACATCCCCCACCCTCAACCCCTGATGCCCATCCGCCAGCCATTCCACCCT 660
        |||
Db    601 CCCCACATCCCCCACCCTCAACCCCTGATGCCCATCCGCCAGCCATTCCACCCT 660

Qy    661 CACCCCCACCCCCACCCCCACGCCCCTCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720
        |||
Db    661 CACCCCCACCCCCACCCCCACGCCCCTCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720

Qy    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
        |||
Db    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
```

Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCTACTCCGTACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCTACTCCGTACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGAGGGTT	1740

Db	1681	 CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640

Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540

Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440

Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400

```

Db      5341  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 5400
           TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA
Qy      5401  TCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401  TCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      5581  GTGGAGTGTCATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581  GTGGAGTGTCATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
           ||||||||||||||||||||||||||||||
Db      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 3

US-08-299-849B-8

; Sequence 8, Application US/08299849B

; Patent No. 5612201

; GENERAL INFORMATION:

; APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;

; APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;

; APPLICANT: Chomez, Patrick

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In

; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor

; NUMBER OF SEQUENCES: 48

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/299,849B

; FILING DATE: 1-SEPTEMBER-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/037,230

; FILING DATE: 26-MARCH-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/04354

; FILING DATE: 22-MAY-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/807,043

; FILING DATE: 12-DECEMBER-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/764,364

```

; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5612201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-299-849B-8

```

```

Query Match          100.0%; Score 5674; DB 2; Length 5674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
        |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
        |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
        |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

```

Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440

Db	1381	 GGTTTGGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	 TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCCAAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	 ACTGAGGAGGCACACACCCCAAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	 CCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	 CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	 GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	 ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	 CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	 TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	 TGCGAGATGAGGGAGGCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	 GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340

Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATTTGGATTTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATTTGGATTTCTCAG	3240

Qy	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140

Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCAC TAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCAC TAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGT CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGT CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTG CAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTG CAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCATG GGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCATG GGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100

```

Db      5041  |||TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAAGGG 5100
Qy      5101  TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
Db      5101  |||TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
Qy      5161  AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA 5220
Db      5161  |||AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA 5220
Qy      5221  AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280
Db      5221  |||AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280
Qy      5281  ATTTTTAAAGATATATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
Db      5281  |||ATTTTTAAAGATATATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
Qy      5341  TAAATCTGAATAAAGAATTCCTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
Db      5341  |||TAAATCTGAATAAAGAATTCCTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
Qy      5401  TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Db      5401  |||TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Qy      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Db      5461  |||CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Db      5521  |||CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
Db      5581  |||GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
Qy      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
Db      5641  |||GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 4

US-08-560-024-1

; Sequence 1, Application US/08560024

; Patent No. 5843448

; GENERAL INFORMATION:

; APPLICANT: Chen, Yao-Tseng; Stockert, Elisabeth;

; APPLICANT: Chen, Yachi; Garin-Chesa, Pilar; Rettig, Wolfgang J.;

; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry;

; APPLICANT: Old, Lloyd J.

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES WHICH BIND TO

; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSOR MAGE-1, RECOMBINANT MAGE-1

; TITLE OF INVENTION: AND MAGE-1 DERIVED IMMUNOGENIC PEPTIDES

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

```

; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,024
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,411
; FILING DATE: 01-FEBRUARY-1994
; APPLICATION NUMBER: 037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5843448man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5354
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-560-024-1

```

```

Query Match          100.0%;  Score 5674;  DB 2;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy      61 ATCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db      61 ATCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

```

Qy	121	CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Db	121	CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Qy	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Db	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080

Db	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081		GCAGGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081		GCAGGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTTCGCATTCCCATTCCCACCCAACC	1200
Db	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTTCGCATTCCCATTCCCACCCAACC	1200
Qy	1201		CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201		CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Db	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Qy	1321		CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321		CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381		GGTTTGGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381		GGTTTGGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441		TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441		TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501		ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501		ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561		ACTGAGGAGGCACACACCCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561		ACTGAGGAGGCACACACCCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621		CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCGTCCTGCTC	1680
Db	1621		CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCGTCCTGCTC	1680
Qy	1681		CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGCAGGGTT	1740
Db	1681		CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGCAGGGTT	1740
Qy	1741		GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741		GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801		ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801		ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861		CCACTCACATTCCCATACCTACCCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861		CCACTCACATTCCCATACCTACCCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921		TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980

Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880

Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780

Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740

Db	4681	 CCAAGGGCCCTCGCTGAAACCAAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCCTTCT	5640

```

Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
          |||||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 5

US-08-142-368A-8

; Sequence 8, Application US/08142368A

; Patent No. 5925729

; GENERAL INFORMATION:

; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;

; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;

; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia

; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor

; TITLE OF INVENTION: Rejection Antigens and Uses Thereof

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/142,368A

; FILING DATE: 02-MAY-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/04354

; FILING DATE: 22-MAY-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/807,043

; FILING DATE: 12-DECEMBER-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/764,364

; FILING DATE: 23-SEPTEMBER-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/728,838

; APPLICATION NUMBER: 9-JULY-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/705,702

; FILING DATE: 23-May-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 5925729man D.

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LUD 5253.4-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5674 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-142-368A-8

Query Match 100.0%; Score 5674; DB 2; Length 5674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
      |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
      |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
      |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGGAGCGTCCAGGCTCTGCCAGACAT 480
      |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGGAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
      |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCCTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
      |||
Db    541 CCCCCTCCAATGCTCACTCCCCTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Qy    601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT 660
      |||
Db    601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT 660

Qy    661 CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG 720
      |||
Db    661 CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG 720

Qy    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
      |||
Db    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
```

Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740

Db	1681		1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640

Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGCTCGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGCTCGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540

Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCA	4440

Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400

```

Db      5341  |||||TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
Qy      5401  TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Db      5401  |||||TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Qy      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Db      5461  |||||CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Db      5521  |||||CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
Db      5581  |||||GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
Qy      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
Db      5641  |||||GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 6

US-08-967-727-8

; Sequence 8, Application US/08967727

; Patent No. 6025474

; GENERAL INFORMATION:

; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;

; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For

; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/967,727

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/037,230

; FILING DATE: 26-MARCH-1993

; APPLICATION NUMBER: PCT/US92/04354

; FILING DATE: 22-MAY-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/807,043

; FILING DATE: 12-DECEMBER-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/764,365

; FILING DATE: 23-SEPTEMBER-1991

; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-08-967-727-8

```

```

Query Match          100.0%; Score 5674; DB 3; Length 5674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CCCGGGGCACCACCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCACCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCACCCCTG 120
        |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db    121 CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
        |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
        |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
        |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
        |||

```

Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCCTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCCACCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Db	601	CCCCACATCCCCCACCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Qy	661	CACCCCCACCCCCACCCCCACGCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCCACCCCCACGCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440

Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCC TAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCC TAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340

Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCC TGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCC TGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCAACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCAACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTTGGATTTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTTGGATTTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300

Db	3241	 ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTG	3360
Db	3301	 CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Db	3361	 GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	 CTTCCTGGAGCTCCAGGAACCCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	 ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	 GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	 TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	 CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721	 GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	 AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	 CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	 TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	 TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCTGAGTCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200

Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCAC TAAGAAGGTGGC	4200
QY	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
QY	4261	AATGCTGGAGAGTGT CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGT CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
QY	4321	CTCTGAGTCCTTG CAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTG CAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
QY	4381	CTCCTATGTCCTTG TCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTG TCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
QY	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
QY	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
QY	4561	GGAGCACAGTGCC TATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCC TATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
QY	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
QY	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
QY	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
QY	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
QY	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
QY	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
QY	4981	TATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
QY	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100

Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTCTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTCTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
Qy	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674
Db	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674

RESULT 7

US-08-037-230D-8

; Sequence 8, Application US/08037230D

; Patent No. 6235525

; GENERAL INFORMATION:

; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;

; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For

; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

```

;   OPERATING SYSTEM:  PC-DOS
;   SOFTWARE:  Wordperfect
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/037,230D
;   FILING DATE:  26-MARCH-1993
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US92/04354
;   FILING DATE:  22-MAY-1992
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  07/807,043
;   FILING DATE:  12-DECEMBER-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  07/764,364
;   FILING DATE:  23-SEPTEMBER-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  07/728,838
;   FILING DATE:  9-JULY-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  07/705,702
;   FILING DATE:  23-MAY-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Hanson, No. 6235525man D.
;   REGISTRATION NUMBER:  30,946
;   REFERENCE/DOCKET NUMBER:  LUD 5353
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 688-9200
;   TELEFAX:  (212) 838-3884
;   INFORMATION FOR SEQ ID NO:  8:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  5674 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  genomic DNA
;   FEATURE:
;   NAME/KEY:  MAGE-1 gene
US-08-037-230D-8

```

```

Query Match          100.0%;  Score 5674;  DB 3;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

```

```

Qy      1  CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC  60

Qy     61  ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61  ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG  120

Qy    121  CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121  CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG  180

Qy    181  TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181  TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG  240

Qy    241  CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||

```

Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Qy	661	CACCCCCACCCCAACCCCAACCCCACTCCCAACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCAACCCCAACCCCACTCCCAACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200

Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCGTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCGTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100

Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCACTAGAGGGAGCGTCCCAGGCC	3060

Db	3001		ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061		CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061		CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121		GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121		GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181		GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGTTCTCAG	3240
Db	3181		GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGTTCTCAG	3240
Qy	3241		ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241		ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301		CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301		CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361		GTAGACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT	3420
Db	3361		GTAGACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT	3420
Qy	3421		CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421		CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481		ACAGAGCAGAGGATGCACAGGGGTGTCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481		ACAGAGCAGAGGATGCACAGGGGTGTCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541		GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541		GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601		TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601		TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661		CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661		CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721		GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721		GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Qy	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960

Db 3901 TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG 3960
 Qy 3961 TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCTGGAGGAGGTGCC 4020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3961 TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCTGGAGGAGGTGCC 4020
 Qy 4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC 4080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC 4080
 Qy 4081 CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG 4140
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4081 CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG 4140
 Qy 4141 GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC 4200
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4141 GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC 4200
 Qy 4201 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA 4260
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4201 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA 4260
 Qy 4261 AATGCTGGAGAGTGTCTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC 4320
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4261 AATGCTGGAGAGTGTCTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC 4320
 Qy 4321 CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA 4380
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4321 CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA 4380
 Qy 4381 CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA 4440
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4381 CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA 4440
 Qy 4441 GATCATGCCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG 4500
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4441 GATCATGCCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG 4500
 Qy 4501 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG 4560
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4501 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG 4560
 Qy 4561 GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA 4620
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4561 GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA 4620
 Qy 4621 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT 4680
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4621 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT 4680
 Qy 4681 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4681 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740
 Qy 4741 GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG 4800
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4741 GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG 4800
 Qy 4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT 4860
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT 4860

Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAATAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAATAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640
Qy	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674
Db	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674

RESULT 8
 US-09-583-850-8
 ; Sequence 8, Application US/09583850

```

; Patent No. 6498021
; GENERAL INFORMATION:
; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/583,850
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/583,613
; FILING DATE:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6498021man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-09-583-850-8

```

```

Query Match          100.0%;  Score 5674;  DB 3;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

Qy 1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
 ||| 60
 Db 1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy 61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
 ||| 120
 Db 61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy 121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
 ||| 180
 Db 121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy 181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
 ||| 240
 Db 181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy 241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
 ||| 300
 Db 241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy 301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
 ||| 360
 Db 301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy 361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
 ||| 420
 Db 361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy 421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
 ||| 480
 Db 421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy 481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
 ||| 540
 Db 481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy 541 CCCCCTCCAATGCTCACTCCCCTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
 ||| 600
 Db 541 CCCCCTCCAATGCTCACTCCCCTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Qy 601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT 660
 ||| 660
 Db 601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT 660

Qy 661 CACCCCCACCCCAACCCCAAGCCAGGATCCGGTTCCCG 720
 ||| 720
 Db 661 CACCCCCACCCCAACCCCAAGCCAGGATCCGGTTCCCG 720

Qy 721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
 ||| 780
 Db 721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780

Qy 781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840
 ||| 840
 Db 781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840

Qy 841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA 900
 ||| 900
 Db 841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA 900

Qy 901 GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA 960

Db	901	 GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	 CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	 GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATCCCCACCCAACC	1200
Db	1141	 CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	 CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	 ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	 CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAAACCACTGACT	1440
Db	1381	 GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	 TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	 ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	 CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	 CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCGGCATTAGGGTCAGG	1800
Db	1741	 GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860

Db 1801 ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC 1860

Qy 1861 CCACTCACATTCCCATACCTACCCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG 1920
 |||

Db 1861 CCACTCACATTCCCATACCTACCCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG 1920

Qy 1921 TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA 1980
 |||

Db 1921 TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA 1980

Qy 1981 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC 2040
 |||

Db 1981 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC 2040

Qy 2041 TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG 2100
 |||

Db 2041 TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG 2100

Qy 2101 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160
 |||

Db 2101 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160

Qy 2161 GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT 2220
 |||

Db 2161 GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT 2220

Qy 2221 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG 2280
 |||

Db 2221 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG 2280

Qy 2281 GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC 2340
 |||

Db 2281 GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC 2340

Qy 2341 TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG 2400
 |||

Db 2341 TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG 2400

Qy 2401 AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT 2460
 |||

Db 2401 AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT 2460

Qy 2461 TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA 2520
 |||

Db 2461 TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA 2520

Qy 2521 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCT 2580
 |||

Db 2521 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCT 2580

Qy 2581 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT 2640
 |||

Db 2581 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT 2640

Qy 2641 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAGGGGTGAGCCCTGGACACC 2700
 |||

Db 2641 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAGGGGTGAGCCCTGGACACC 2700

Qy 2701 TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT 2760
 |||

Db 2701 TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT 2760

Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660

Qy 3661 CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG 3720
 |||
 Db 3661 CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG 3720

Qy 3721 GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC 3780
 |||
 Db 3721 GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC 3780

Qy 3781 AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT 3840
 |||
 Db 3781 AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT 3840

Qy 3841 CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG 3900
 |||
 Db 3841 CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG 3900

Qy 3901 TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG 3960
 |||
 Db 3901 TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG 3960

Qy 3961 TGTGCAGGCTGCCACCTCCTCCTCTCTCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC 4020
 |||
 Db 3961 TGTGCAGGCTGCCACCTCCTCCTCTCTCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC 4020

Qy 4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC 4080
 |||
 Db 4021 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC 4080

Qy 4081 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG 4140
 |||
 Db 4081 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG 4140

Qy 4141 GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC 4200
 |||
 Db 4141 GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC 4200

Qy 4201 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA 4260
 |||
 Db 4201 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA 4260

Qy 4261 AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC 4320
 |||
 Db 4261 AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC 4320

Qy 4321 CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA 4380
 |||
 Db 4321 CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA 4380

Qy 4381 CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA 4440
 |||
 Db 4381 CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA 4440

Qy 4441 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG 4500
 |||
 Db 4441 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG 4500

Qy 4501 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG 4560
 |||
 Db 4501 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG 4560

Qy 4561 GGAGCACAGTGCCATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA 4620

Db	4561	 GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATGTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATGTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520

```

Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
        |||||
Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
        |||||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        |||||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 9

US-09-579-197-8

; Sequence 8, Application US/09579197

; Patent No. 6552180

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Beatrice; Van den Eynde, Benoit;

; van der Bruggen, Pierre; Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding

; For Tumor Rejection Antigen Precursor Mage-3 And Uses The

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

; STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/579,197

; FILING DATE: 26-May-2000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/037,230

; FILING DATE:

; APPLICATION NUMBER: 07/807,043

; FILING DATE: 12-DECEMBER-1991

; APPLICATION NUMBER: 07/764,364

; FILING DATE: 23-SEPTEMBER-1991

; APPLICATION NUMBER: 07/728,838

; FILING DATE: 9-JULY-1991

; APPLICATION NUMBER: 07/705,702

; FILING DATE: 23-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 6552180man D.

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LUD 5353

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5674 base pairs

```

;          TYPE: nucleic acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;          MOLECULE TYPE: genomic DNA
;          FEATURE:
;          . NAME/KEY:  MAGE-1 gene
;          SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-579-197-8

```

```

Query Match          100.0%;  Score 5674;  DB 3;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1  CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db      1  CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61  ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61  ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121  CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121  CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181  TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db    181  TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241  CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
      |||
Db    241  CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301  AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
      |||
Db    301  AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361  TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
      |||
Db    361  TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421  CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
      |||
Db    421  CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481  CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCCTGACCCCAAC 540
      |||
Db    481  CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCCTGACCCCAAC 540

Qy    541  CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCA 600
      |||
Db    541  CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCA 600

Qy    601  CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT 660
      |||
Db    601  CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT 660

Qy    661  CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCTCCG 720
      |||
Db    661  CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCTCCG 720

```

Qy 721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
 |||
 Db 721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780

Qy 781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840
 |||
 Db 781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840

Qy 841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA 900
 |||
 Db 841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA 900

Qy 901 GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA 960
 |||
 Db 901 GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA 960

Qy 961 CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC 1020
 |||
 Db 961 CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC 1020

Qy 1021 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG 1080
 |||
 Db 1021 TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG 1080

Qy 1081 GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC 1140
 |||
 Db 1081 GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC 1140

Qy 1141 CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC 1200
 |||
 Db 1141 CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC 1200

Qy 1201 CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC 1260
 |||
 Db 1201 CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTACCTGACCACC 1260

Qy 1261 ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC 1320
 |||
 Db 1261 ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC 1320

Qy 1321 CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC 1380
 |||
 Db 1321 CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC 1380

Qy 1381 GGTTCGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT 1440
 |||
 Db 1381 GGTTCGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT 1440

Qy 1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCGAGGGGCGGCTTGAG 1500
 |||
 Db 1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCGAGGGGCGGCTTGAG 1500

Qy 1501 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560
 |||
 Db 1501 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560

Qy 1561 ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG 1620
 |||
 Db 1561 ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG 1620

Qy 1621 CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC 1680

Db	1621		CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681		CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681		CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741		GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741		GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801		ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801		ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861		CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861		CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921		TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Db	1921		TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981		GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981		GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041		TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041		TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101		ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101		ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161		GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161		GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221		GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221		GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281		GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281		GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341		TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341		TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401		AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401		AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461		TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461		TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521		CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580

Db 2521 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT 2580
 Qy 2581 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT 2640
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2581 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT 2640
 Qy 2641 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGGTCAGCCCTGGACACC 2700
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2641 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGGTCAGCCCTGGACACC 2700
 Qy 2701 TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT 2760
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2701 TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT 2760
 Qy 2761 CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG 2820
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2761 CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG 2820
 Qy 2821 GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG 2880
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2821 GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG 2880
 Qy 2881 GACCAGAACACTGAGGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTGTCACCCAGAG 2940
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2881 GACCAGAACACTGAGGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTGTCACCCAGAG 2940
 Qy 2941 AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG 3000
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 2941 AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG 3000
 Qy 3001 ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC 3060
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3001 ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC 3060
 Qy 3061 CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT 3120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3061 CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT 3120
 Qy 3121 GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT 3180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3121 GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT 3180
 Qy 3181 GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG 3240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3181 GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG 3240
 Qy 3241 ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA 3300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3241 ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA 3300
 Qy 3301 CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG 3360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3301 CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG 3360
 Qy 3361 GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT 3420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3361 GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT 3420
 Qy 3421 CTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC 3480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 3421 CTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC 3480

Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380

Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTTCCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTTCCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340

```

Db      5281  |||||||||||||||||||||||||||||||||||||||||||||||||||||| 5340
          ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT
Qy      5341  TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341  TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      5401  TCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATA 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401  TCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATA 5460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCTTCT 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCTTCT 5640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
          ||||||||||||||||||||||||||||||||||
Db      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

```

RESULT 10
US-09-404-026-8
; Sequence 8, Application US/09404026
; Patent No. 6565857
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/404,026
; FILING DATE: 23-SEPT-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043

```

```

; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6565857man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
US-09-404-026-8

```

```

Query Match          100.0%; Score 5674; DB 3; Length 5674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
        |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
        |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

```

Db	421		CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601		CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Db	601		CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Qy	661		CACCCCCACCCCAACCCCAAGCCCACTCCCAACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Db	661		CACCCCCACCCCAACCCCAAGCCCACTCCCAACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Qy	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781		GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781		GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901		GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901		GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961		CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Db	961		CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Qy	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Db	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Qy	1201		CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201		CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321		CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380

Db 1321 CCCACCCATCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC 1380

Qy 1381 GGT TTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT 1440
 |||

Db 1381 GGT TTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT 1440

Qy 1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAG 1500
 |||

Db 1441 TGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAG 1500

Qy 1501 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560
 |||

Db 1501 ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG 1560

Qy 1561 ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG 1620
 |||

Db 1561 ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG 1620

Qy 1621 CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC 1680
 |||

Db 1621 CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC 1680

Qy 1681 CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGAGGGTT 1740
 |||

Db 1681 CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGAGGGTT 1740

Qy 1741 GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCCGATTAGGGTCAGG 1800
 |||

Db 1741 GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCCGATTAGGGTCAGG 1800

Qy 1801 ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC 1860
 |||

Db 1801 ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC 1860

Qy 1861 CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG 1920
 |||

Db 1861 CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG 1920

Qy 1921 TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCAC'TCGGATCTTGACGTCCCCATCCA 1980
 |||

Db 1921 TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCAC'TCGGATCTTGACGTCCCCATCCA 1980

Qy 1981 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC 2040
 |||

Db 1981 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC 2040

Qy 2041 TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG 2100
 |||

Db 2041 TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG 2100

Qy 2101 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160
 |||

Db 2101 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG 2160

Qy 2161 GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT 2220
 |||

Db 2161 GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT 2220

Qy 2221 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG 2280
 |||

Db 2221 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG 2280

Qy	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180

Qy	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGATTCTT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGATTCTT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTAGTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCTGGGCACCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCTGGGCACCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140

Db	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141		GCCAAGCACCTCTTGTATCCTGGAGTCCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141		GCCAAGCACCTCTTGTATCCTGGAGTCCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261		AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261		AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321		CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321		CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381		CTCCTATGTCTTGTTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381		CTCCTATGTCTTGTTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501		CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501		CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561		GGAGCACAGTGCCATGAGGAGGCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA	4620
Db	4561		GGAGCACAGTGCCATGAGGAGGCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA	4620
Qy	4621		GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621		GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681		CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681		CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741		GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741		GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801		GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801		GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861		CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861		CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921		GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921		GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981		TATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040

```

Db      4981 TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC 5040
Qy      5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG 5100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG 5100
Qy      5101 TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5101 TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
Qy      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA 5220
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA 5220
Qy      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA 5280
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA 5280
Qy      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
Qy      5341 TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
Qy      5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC 5460
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC 5460
Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTTCCTTCT 5640
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTTCCTTCT 5640
Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        ||||||||||||||||||||||||||||||||||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

```

RESULT 11
US-09-312-464-8
; Sequence 8, Application US/09312464
; Patent No. 6599699
;   GENERAL INFORMATION:
;       APPLICANT: Van den Eynde, Benoit; van der Bruggen, Pierre;
;               Boon-Falleu, Thierry
;       TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING FOR
;               TUMOR REJECTION ANTIGEN PRECURSOR MAGE-2 AND USES THEREOF
;       NUMBER OF SEQUENCES: 28
;       CORRESPONDENCE ADDRESS:
;               ADDRESSEE: Fulbright & Jaworski LLP
;               STREET: 666 Fifth Avenue
;               CITY: New York City

```

```

; STATE: New York
; COUNTRY:
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/312,464
; FILING DATE: 17-May-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/967,727
; FILING DATE: 27-NOVEMBER-1997
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6599699man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5253.5-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)318-3168
; TELEFAX: (212)752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-312-464-8

```

```

Query Match          100.0%;  Score 5674;  DB 3;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

```

Qy	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Db	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080

Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040

Db	1981	 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	 TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	 GTGGGACCCAGGCCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	 GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	 TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	 AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	 TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Db	2641	 GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	 TCACCCAGGATGTGGCTTCTTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	 CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	 GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCAGAG	2940

Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCCTCCTGTCCTTCCATTCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Db	3181	GTCCCCCTCCTGTCCTTCCATTCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAATTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAATTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840

Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGAGGCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGAGGCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740

Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGCCCTTTGAGAATGTAAGAGAAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGCCCTTTGAGAATGTAAGAGAAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
Qy	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674

|||||
Db 5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

RESULT 12

US-09-583-848A-8

; Sequence 8, Application US/09583848A

; Patent No. 6946289

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Beatrice; Van den Eynde, Benoit; van der Bruggen,
; Pierre; Boon-Falleur, Thierry

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For Tumor
; Rejection Antigen Precursor Mage-3 And Uses Thereof

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fulbright & Jaworski L.L.P.

; STREET: 666 Fifth Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/583,848A

; FILING DATE: 31-May-2000

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US92/04354

; FILING DATE: 22-MAY-1992

; APPLICATION NUMBER: 07/807,043

; FILING DATE: 12-DECEMBER-1991

; APPLICATION NUMBER: 07/764,364

; FILING DATE: 23-SEPTEMBER-1991

; APPLICATION NUMBER: 07/728,838

; FILING DATE: 9-JULY-1991

; APPLICATION NUMBER: 07/705,702

; FILING DATE: 23-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 6946289man D.

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LUD 5353

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5674 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA

; FEATURE:

; NAME/KEY: MAGE-1 gene

; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-09-583-848A-8

Query Match 100.0%; Score 5674; DB 3; Length 5674;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
      |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
      |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCAC TGGGGACTCGAAGTCAGAG 420
      |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCAC TGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
      |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
      |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCA 600
      |||
Db    541 CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCA 600

Qy    601 CCCACATCCCCACCCCATCCCTCAACCTGATGCCATCCGCCAGCCATTCCACCCT 660
      |||
Db    601 CCCACATCCCCACCCCATCCCTCAACCTGATGCCATCCGCCAGCCATTCCACCCT 660

Qy    661 CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCTCG 720
      |||
Db    661 CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCTCG 720

Qy    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
      |||
Db    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780

Qy    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840
      |||
Db    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840

Qy    841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA 900
      |||
```

Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800

Qy	1801	ACCCTGGGAGGGAAC TGAGGGT TCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGT TCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTGAGCCCTGGACACC	2700

Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGAAGTCAAGTACAGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGAAGTCAAGTACAGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCACAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCACAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660

Db	3601	 TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	 CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721	 GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	 AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	 CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	 TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	 TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	 CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	 CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	 GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	 AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	 CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	 CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560

Db 4501 CCATGCTCCTGAGGAGGAAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG 4560

Qy 4561 GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAA 4620
|||||

Db 4561 GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAA 4620

Qy 4621 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT 4680
|||||

Db 4621 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT 4680

Qy 4681 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740
|||||

Db 4681 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT 4740

Qy 4741 GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG 4800
|||||

Db 4741 GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG 4800

Qy 4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT 4860
|||||

Db 4801 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT 4860

Qy 4861 CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT 4920
|||||

Db 4861 CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT 4920

Qy 4921 GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT 4980
|||||

Db 4921 GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT 4980

Qy 4981 TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC 5040
|||||

Db 4981 TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC 5040

Qy 5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG 5100
|||||

Db 5041 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG 5100

Qy 5101 TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
|||||

Db 5101 TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160

Qy 5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA 5220
|||||

Db 5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA 5220

Qy 5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280
|||||

Db 5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280

Qy 5281 ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
|||||

Db 5281 ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340

Qy 5341 TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
|||||

Db 5341 TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400

Qy 5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC 5460
|||||

Db 5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC 5460

```

Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
          |||
Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520

Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
          |||
Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580

Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
          |||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
          |||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 13

US-09-949-016-12445

; Sequence 12445, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12445

; LENGTH: 5699

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-12445

```

Query Match          69.3%;  Score 3934.8;  DB 3;  Length 5699;
Best Local Similarity 99.8%;  Pred. No. 0;
Matches 4002;  Conservative 0;  Mismatches 2;  Indels 6;  Gaps 6;

```

```

Qy      1669 CCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGAC 1728
          |||
Db      1 CCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGAC 60

Qy      1729 CGGGGCAGGGTTGGTCAGGAGA-GGCAGGGCCCAGGCATCAAGGTCCA-GCATCCGCCCCG 1786
          |||
Db      61 CGGGGCAGGGTTGGTCAGGAGAGGGCAGGGCCCAGGCATCAAGGTCCAGGCATCCGCCCCG 120

Qy      1787 GCATTAGGGTCAGGACCCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCA 1846
          |||
Db      121 GCATTAGGGTCAGGACCCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCA 180

Qy      1847 TCTCCACCGCCACCCCACTCACATTCCCATACTACCCCTACCCCCAACCTCATCTTGT 1906
          |||

```

Db 181 TCTCCACCGCCACCCCACTCACATTCCCATACTACCCCTACCCCCAACCTCATCTTGT 240
 Qy 1907 CAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTT 1966
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 CAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTT 300
 Qy 1967 GACGTCCCCATCCAGGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAG 2026
 |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
 Db 301 GACGTCCCCATCCAGGG-CTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAG 359
 Qy 2027 AGGGAGGGGCCCTACTGCGAGATGAGGGAGGCTCAGAGGACCCAGCACCCCTAGGACACCG 2086
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 360 AGGGAGGGGCCCTACTGCGAGATGAGGGAGGCTCAGAGGACCCAGCACCCCTAGGACACCG 419
 Qy 2087 CACCCCTGTCTGAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACT 2146
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 420 CACCCCTGTCTGAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAAATGATGGGGACT 479
 Qy 2147 CAGATT-GCATGGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAG 2205
 ||||| ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 480 CAGATTAGCATGGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAG 539
 Qy 2206 GACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCA 2265
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 540 GACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCA 599
 Qy 2266 CGGTGGCCACATATGGCCCATATTTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGT 2325
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 600 CGGTGGCCACATATGGCCCATATTTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGT 659
 Qy 2326 CTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGA 2385
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 660 CTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGA 719
 Qy 2386 TGTGCCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAG 2445
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 720 TGTGCCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAG 779
 Qy 2446 TCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCA 2505
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 780 TCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCA 839
 Qy 2506 TTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGT 2565
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 840 TTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGT 899
 Qy 2566 AAAGGGGGGATGTCTACTCATGTTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCA 2625
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 900 AAAGGGGGGATGTCTACTCATGTTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCA 959
 Qy 2626 GGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAAGGGG 2685
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 960 GGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCTCACCCAGAACCAAAGGGG 1019
 Qy 2686 TCAGCCCTGGACACCTCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGG 2745
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1020 TCAGCCCTGGACACCTCACCCAGGATGTGGCTTC-TTTTCACTCCTGTTTCCAGATCTGG 1078
 Qy 2746 GGCAGGTGAGGACCTCATTTCTCAGAGGGTGAAGTCAAGTACGTTAGGGACCCCATCTGG 2805
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1079 GGCAGGTGAGGACCTCATTTCTCAGAGGGTGAAGTCAAGTACGTTAGGGACCCCATCTGG 1138

Qy	2806	TCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGA	2865
Db	1139	TCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGA	1198
Qy	2866	CTGAGGGTACCCCAGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCCT	2925
Db	1199	CTGAGGGTACCCCAGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCCT	1258
Qy	2926	GCTGTCACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGTCTTCCGTTATCCTGGGA	2985
Db	1259	GCTGTCACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGTCTTCCGTTATCCTGGGA	1318
Qy	2986	TCATTGATGTCAGGGACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAG	3045
Db	1319	TCATTGATGTCAGGGACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAG	1378
Qy	3046	GGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGA	3105
Db	1379	GGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGA	1438
Qy	3106	CACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACG	3165
Db	1439	CACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACG	1498
Qy	3166	TGTGGCCAGATGTTTGTCCCCCTCCTGTCCTTCCATTCCATTATCATGGATGTGAACCTTG	3225
Db	1499	TGTGGCCAGATGTTTGTCCCCCTCCTGTCCTTCCATTCCATTATCATGGATGTGAACCTTG	1558
Qy	3226	ATTTGGATTTCTCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAG	3285
Db	1559	ATTTGGATTTCTCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAG	1618
Qy	3286	GGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTC	3345
Db	1619	GGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTC	1678
Qy	3346	CAGCCCACCTCCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCCTGTCACCCCTGAG	3405
Db	1679	CAGCCCACCTCCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCCTGTCACCCCTGAG	1738
Qy	3406	GGCCCGTGGATTCTCTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGA	3465
Db	1739	GGCCCGTGGATTCTCTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGA	1798
Qy	3466	CAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCC	3525
Db	1799	CAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCC	1858
Qy	3526	CTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGC	3585
Db	1859	CTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGC	1918
Qy	3586	CTCACCTCCCTACTGTCAGTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGT	3645
Db	1919	CTCACCTCCCTACTGTCAGTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGT	1978
Qy	3646	ACCCTCTCACTTCCTCCTTCAGGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCC	3705
Db	1979	ACCCTCTCACTTCCTCCTTCAGGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCC	2038

Qy	3706	CTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCCTTGTAGAGTCTC	3765
Db	2039	CTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCCTTGTAGAGTCTC	2098
Qy	3766	CAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGT	3825
Db	2099	CAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGT	2158
Qy	3826	CTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTC	3885
Db	2159	CTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTC	2218
Qy	3886	TCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGC	3945
Db	2219	TCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGC	2278
Qy	3946	CCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCTGGGCAC	4005
Db	2279	CCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCTGGGCAC	2338
Qy	4006	CCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTC	4065
Db	2339	CCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTC	2398
Qy	4066	CGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAG	4125
Db	2399	CGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAG	2458
Qy	4126	CCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAAT	4185
Db	2459	CCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAAT	2518
Qy	4186	CACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCC	4245
Db	2519	CACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCC	2578
Qy	4246	AGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTCTGA	4305
Db	2579	AGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTCTGA	2638
Qy	4306	GATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGC	4365
Db	2639	GATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGC	2698
Qy	4366	AGACCCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCT	4425
Db	2699	AGACCCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCT	2758
Qy	4426	GCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGAT	4485
Db	2759	GCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGAT	2818
Qy	4486	TGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGA	4545
Db	2819	TGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGA	2878
Qy	4546	GGTGTATGATGGGAGGGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCCAAGA	4605
Db	2879	GGTGTATGATGGGAGGGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCCAAGA	2938
Qy	4606	TTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTA	4664

Db	2939	TTTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCACGCTA	2998
Qy	4665	TGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTA	4724
Db	2999	TGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTA	3058
Qy	4725	TGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTT	4784
Db	3059	TGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTT	3118
Qy	4785	GAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGAC	4844
Db	3119	GAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGAC	3178
Qy	4845	TGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAG	4904
Db	3179	TGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAG	3238
Qy	4905	GCCCATTCTTCACTCTGAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATT	4964
Db	3239	GCCCATTCTTCACTCTGAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATT	3298
Qy	4965	GGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTAAG	5024
Db	3299	GGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAATTGTTCAAATGTTTTTTTTTAAG	3358
Qy	5025	GGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGT	5084
Db	3359	GGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGT	3418
Qy	5085	GTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTT	5144
Db	3419	GTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTT	3478
Qy	5145	TGTGAATTGGGATAATAACAGCAGTGGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGT	5204
Db	3479	TGTGAATTGGGATAATAACAGCAGTGGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGT	3538
Qy	5205	AAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCT	5264
Db	3539	AAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCT	3598
Qy	5265	CAGTCTATTCTGTAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTG	5324
Db	3599	CAGTCTATTCTGTAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTG	3658
Qy	5325	AGAATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCTGTTCAGTGGCTCTTTTCTT	5384
Db	3659	AGAATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCTGTTCAGTGGCTCTTTTCTT	3718
Qy	5385	CTCCATGCACTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGG	5444
Db	3719	CTCCATGCACTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGG	3778
Qy	5445	TAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGCTTAGGAGCTGCAGTCACGTAATC	5504
Db	3779	TAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGCTTAGGAGCTGCAGTCACGTAATC	3838
Qy	5505	GAGGTGGCAAGATGTCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGG	5564

```

Db      3839 GAGGTGGCAAGATGTCCTCTAAAGATGTAGGAAAAGTGAGAGAGGGGTGAGGGTGTGGG 3898
Qy      5565 GCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGA 5624
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3899 GCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGA 3958
Qy      5625 AACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3959 AACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 4008

```

RESULT 14

```

US-09-949-016-14430
; Sequence 14430, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14430
; LENGTH: 5699
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14430

```

```

Query Match          69.3%; Score 3934.8; DB 3; Length 5699;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4002; Conservative 0; Mismatches 2; Indels 6; Gaps 6;

```

```

Qy      1669 CCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGAC 1728
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGAC 60
Qy      1729 CGGGGCAGGGTTGGTCAGGAGA-GGCAGGGCCCAGGCATCAAGGTCCA-GCATCCGCCCCG 1786
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGGGGCAGGGTTGGTCAGGAGAGGGCAGGGCCCAGGCATCAAGGTCCAGGCATCCGCCCCG 120
Qy      1787 GCATTAGGGTCAGGACCTGGGAGGGAAGTGGAGGGTTCCCCACCCACACCTGTCTCCTCA 1846
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GCATTAGGGTCAGGACCTGGGAGGGAAGTGGAGGGTTCCCCACCCACACCTGTCTCCTCA 180
Qy      1847 TCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGT 1906
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGT 240
Qy      1907 CAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTT 1966
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTT 300
Qy      1967 GACGTCCCCATCCAGGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAG 2026

```

Db	301	 GACGTCCCCATCCAGGG-CTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAG	359
Qy	2027	AGGGAGGGCCCTACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCG	2086
Db	360	 AGGGAGGGCCCTACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCG	419
Qy	2087	CACCCCTGTCTGAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACT	2146
Db	420	 CACCCCTGTCTGAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAAATGATGGGGACT	479
Qy	2147	CAGATT-GCATGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAG	2205
Db	480	 CAGATTAGCATGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAG	539
Qy	2206	GACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCA	2265
Db	540	 GACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCA	599
Qy	2266	CGGTGGCCACATATGGCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGT	2325
Db	600	 CGGTGGCCACATATGGCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGT	659
Qy	2326	CTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGA	2385
Db	660	 CTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGA	719
Qy	2386	TGTGCCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAG	2445
Db	720	 TGTGCCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAG	779
Qy	2446	TCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCA	2505
Db	780	 TCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCA	839
Qy	2506	TTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGT	2565
Db	840	 TTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGT	899
Qy	2566	AAAGGGGGGATGTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCA	2625
Db	900	 AAAGGGGGGATGTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCA	959
Qy	2626	GGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAAGGGG	2685
Db	960	 GGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCTCACCCAGAACCAAAGGGG	1019
Qy	2686	TCAGCCCTGGACACCTCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGG	2745
Db	1020	 TCAGCCCTGGACACCTCACCCAGGATGTGGCTTC-TTTTCACTCCTGTTTCCAGATCTGG	1078
Qy	2746	GGCAGGTGAGGACCTCATTCTCAGAGGGTGAAGTCAACGTAGGGACCCCATCTGG	2805
Db	1079	 GGCAGGTGAGGACCTCATTCTCAGAGGGTGAAGTCAACGTAGGGACCCCATCTGG	1138
Qy	2806	TCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGA	2865
Db	1139	 TCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGA	1198
Qy	2866	CTGAGGGTACCCAGGACCAGAACACTGAGGGGAGACTGCACAGAAATCAGCCCTGCCCT	2925

Db	1199	CTGAGGGTACCCCAGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCCT	1258
Qy	2926	GCTGTCACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGTCC TTCCGTTATCCTGGGA	2985
Db	1259	GCTGTCACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGTCC TTCCGTTATCCTGGGA	1318
Qy	2986	TCATTGATGTCAGGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAG	3045
Db	1319	TCATTGATGTCAGGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAG	1378
Qy	3046	GGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGA	3105
Db	1379	GGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGA	1438
Qy	3106	CACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACG	3165
Db	1439	CACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACG	1498
Qy	3166	TGTGGCCAGATGTTTGTCCCTCCTGTCCTTCCATTCTTATCATGGATGTGAACTCTTG	3225
Db	1499	TGTGGCCAGATGTTTGTCCCTCCTGTCCTTCCATTCTTATCATGGATGTGAACTCTTG	1558
Qy	3226	ATTTGGATTTCTCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAG	3285
Db	1559	ATTTGGATTTCTCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAG	1618
Qy	3286	GGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTC	3345
Db	1619	GGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTC	1678
Qy	3346	CAGCCCACCTCCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTTGAG	3405
Db	1679	CAGCCCACCTCCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTTGAG	1738
Qy	3406	GGCCCGTGGATTCTCTTCTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGA	3465
Db	1739	GGCCCGTGGATTCTCTTCTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGA	1798
Qy	3466	CAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCC	3525
Db	1799	CAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCC	1858
Qy	3526	CTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGC	3585
Db	1859	CTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGC	1918
Qy	3586	CTCACCTCCCTACTGTGTCAGTCTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGT	3645
Db	1919	CTCACCTCCCTACTGTGTCAGTCTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGT	1978
Qy	3646	ACCTCTCACTTCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCC	3705
Db	1979	ACCTCTCACTTCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCC	2038
Qy	3706	CTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTC	3765
Db	2039	CTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTC	2098
Qy	3766	CAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCAGGCCTGTGGGT	3825
Db	2099	CAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCAGGCCTGTGGGT	2158

Qy	3826	CTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTC	3885
Db	2159	CTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTC	2218
Qy	3886	TCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGC	3945
Db	2219	TCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGC	2278
Qy	3946	CCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGGTCTGGGCAC	4005
Db	2279	CCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGGTCTGGGCAC	2338
Qy	4006	CCTGGAGGAGGTGCCCACCTGCTGGGTCAACAGATCCTCCCCAGAGTCTCAGGGAGCCTC	4065
Db	2339	CCTGGAGGAGGTGCCCACCTGCTGGGTCAACAGATCCTCCCCAGAGTCTCAGGGAGCCTC	2398
Qy	4066	CGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAG	4125
Db	2399	CGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAG	2458
Qy	4126	CCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAAT	4185
Db	2459	CCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAAT	2518
Qy	4186	CACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCC	4245
Db	2519	CACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCC	2578
Qy	4246	AGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTCTGA	4305
Db	2579	AGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTCTGA	2638
Qy	4306	GATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGC	4365
Db	2639	GATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGC	2698
Qy	4366	AGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCT	4425
Db	2699	AGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCT	2758
Qy	4426	GCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCTGATAATTGTCCTGGTCATGAT	4485
Db	2759	GCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCTGATAATTGTCCTGGTCATGAT	2818
Qy	4486	TGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGA	4545
Db	2819	TGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGA	2878
Qy	4546	GGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGA	4605
Db	2879	GGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGA	2938
Qy	4606	TTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTA	4664
Db	2939	TTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCACGCTA	2998
Qy	4665	TGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTA	4724
Db	2999	TGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTA	3058

Qy	4725	TGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTT	4784
Db	3059	TGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTT	3118
Qy	4785	GAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGAC	4844
Db	3119	GAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGAC	3178
Qy	4845	TGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAG	4904
Db	3179	TGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAG	3238
Qy	4905	CCCCATTCTTCACTCTGAAGAGAGCGGTCAAGTGTCTCAGTAGTAGGTTTCTGTTCTATT	4964
Db	3239	CCCCATTCTTCACTCTGAAGAGAGCGGTCAAGTGTCTCAGTAGTAGGTTTCTGTTCTATT	3298
Qy	4965	GGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAG	5024
Db	3299	GGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAG	3358
Qy	5025	GGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGT	5084
Db	3359	GGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGT	3418
Qy	5085	GTATATAGTTTTAAGGGTAAGAGTCTTGTGTTTTTATTTCAGATTGGGAAATCCATTCTATTT	5144
Db	3419	GTATATAGTTTTAAGGGTAAGAGTCTTGTGTTTTTATTTCAGATTGGGAAATCCATTCTATTT	3478
Qy	5145	TGTGAATTGGGATAATAACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGT	5204
Db	3479	TGTGAATTGGGATAATAACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGT	3538
Qy	5205	AAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCT	5264
Db	3539	AAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCT	3598
Qy	5265	CAGTCTATTCTGTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTG	5324
Db	3599	CAGTCTATTCTGTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTG	3658
Qy	5325	AGAATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCTGTTCACCTGGCTCTTTTCTT	5384
Db	3659	AGAATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCTGTTCACCTGGCTCTTTTCTT	3718
Qy	5385	CTCCATGCACCTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGG	5444
Db	3719	CTCCATGCACCTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGG	3778
Qy	5445	TAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATC	5504
Db	3779	TAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATC	3838
Qy	5505	GAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGG	5564
Db	3839	GAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGG	3898
Qy	5565	GCTCCGGGTGAGAGTGGTGGAGTGTCATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGA	5624
Db	3899	GCTCCGGGTGAGAGTGGTGGAGTGTCATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGA	3958
Qy	5625	AACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674

Db 3959 AACTGCAGTTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 4008

Query Match 46.8%; Score 2655; DB 3; Length 11495;
Best Local Similarity 73.6%; Pred. No. 0;
Matches 4231; Conservative 0; Mismatches 1100; Indels 416; Gaps 50;

Qy 487 CAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAACCCCCAC 546
 ||||| || ||||| ||||| | ||| | | ||| |||||
 Db 6437 CAGGACCCTAGGAGAGGGCTGAGTGTCCCCA---CCCCATTCTATCCCCTACCCCTT 6493

Qy 547 TCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCACCCAC 606
 ||| || ||||| | || | ||| |
 Db 6494 TCCCATCTGCACTCCC-----TACCCCATCTGTACCCCC 6527

Qy 607 ATCCCCCACCCCATCCCTCAACCCCTGATGCCCATCCGCCAGCCATTCCACCCCTACCCC 666
 || ||||| || || || || || ||||| || |||||
 Db 6528 ATTCCCCACCTGTGCCCTATCCTCCCCAACCCCCAACAGCCTCATACCCCTCCTCCC 6587

Qy 667 CACCCCCACCCCAAGGCCACTCCACCCCAAGGCAGGATCCG-GTTCGCCAGG 725
 ||||| || || ||| | | || | | ||| |||||
 Db 6588 CACCCTACCTTCATCCCATCAGTGCAGCATCCGGTTCACCCCTGCTTCAATCCAGG 6647

Qy 726 AAACATCCGGGTGCCCGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGAGAAGC 785
 || | ||||| ||||| ||||| ||||| | |||| ||| |||||
 Db 6648 CAAGCCCTGGGTGGCCGATGTGATGCCACTGACTTGTGAATTGAGGGTTAGAGAGAAGT 6707

Qy 786 GAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGGCTCTG 845
 ||| || ||||| || || || || || || || || || || ||||| ||
 Db 6708 GAGTTTCTGGGTCTGAAGGGTGGC-TTGAGATCGGCAGAGGAAGGTGGCCAGGCTTTG 6766

Qy 846 TGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATAGAGAG 905
 ||| ||||| ||||| ||||| ||||| | |||| || | || ||||| |
 Db 6767 TGAAGAGGCAAAGTGAGACTCTGAGGGAGGATTAGAGAAACCCCTATCCCTGATAGAGGG 6826

Qy 906 CCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGACGTCT 965
 |||| | ||| | || || || || |||||
 Db 6827 TCCCAGCCCTGGACTACCC-----CGCGGAGGCTGACTTCT 6862

Qy 966 CAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAGCCTTGAGAGACACCAGGTTCTTCTC 1025
 ||| ||||| || || || || || || || || || || ||
 Db 6863 CAGACTGGGCTGCTCCCCACCTCCGCCCC-----TTCGCAACGCGTTTGTTTAAGCCAC 6917

Qy 1026 CCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAGG 1085
 ||||| ||||| ||||| ||||| || || ||||| ||||| |||||
 Db 6918 AGGGGACTCTGGAGTCAGAGGTTGGTGTGATCAGGGAAGGGCTGGTTAGGAGA-GGCATG 6976

Qy 1086 GCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAAG 1145
 || ||||| ||||| ||||| ||||| || || || || |||||
 Db 6977 GCCCAGGCCCTGCCAGGAATCAAAGTCAGAAACC-TGAGAGGGAAGTGGGTCCCCCAAG 7035

Qy 1146 ACTGCACTCCAATCCCCTACCCACCCCATTCGCATTCCCATTCCCCACCCAACCCCAT 1205
 | || || ||||| |||||
 Db 7036 ATCCTAGTCTAACCCCACTCCACAA----- 7062

Qy 1206 CTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACCACCT 1265
 | || | || | || || || || || || |||||
 Db 7063 -----ATCCGCTGCCATTTGCTGCTCCATTTCCATTCTTGCCT 7104

Qy 1266 CCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAACCCAC 1325
 ||| || || ||
 Db 7105 CCACCCTACCA----- 7116

Qy 1326 CCTCATCTCTCTCATGTGCCCCACTCCCATCGCTCCCCATTCTGGCAGAATCCGGTTT 1385
 ||||| ||||| |||||
 Db 7117 -----GGCAGAATCCAGTTC 7131

Qy	1386	GCC-CCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACTTGAA	1444
Db	7132	CCCTTCTGCTATCAATCCAGGGAAACCCAGGCTTGGTGCTGGGATGTTTTT-----	7183
Qy	1445	CCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAGATCC	1504
Db	7184	-----TGGGGGTCAGAGAATCAAGGGCATAGTCCTGAGGGGCCAGTTGAGATCG	7232
Qy	1505	ACTGAGGGGAGTGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGGACTG	1564
Db	7233	GCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAGGCAAGGTGAGACTCTGAGGAAGGACTG	7292
Qy	1565	AGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTGCCAG	1624
Db	7293	AGGAGGCCCCCAACCAAGATAGA-GGAACCCAAATAATCCAGCGCAGCTCCTGCTGCCAG	7351
Qy	1625	CCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCGTCCTGTCCTCCACT	1684
Db	7352	TCTTGGACCACCCGG---GGGAAGACTTCTCA---GGCTAGGCCATCCAGCTCCCACT	7404
Qy	1685	GCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTTGGTC	1744
Db	7405	GCCACTAAAGCTACAGGGGACTCTAGAGTCAAGAGCTTGGTGTGCCCA-----	7452
Qy	1745	AGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGGACCC	1804
Db	7453	-----AGGCAGGGCCAGGC-----TCTGCCTGGCATCGGGGTCAGGACCT	7493
Qy	1805	TGGGAGGGAACCTGAGGGTTCCCAACCCACACCTGTCTCCTCATCTCCACCGCCACCCAC	1864
Db	7494	TGAGAGGGAACCTGAGGGCGCTACACCCCAACCCATCCGCATTC-----CAACAT	7543
Qy	1865	TCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTGTCAA	1924
Db	7544	GCCCAGCCCCATCCCAACTCCGTTTTCAGAGAATCCATTTT---TCCCTGCAGTCAA	7599
Qy	1925	CCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCATCCAGGGT	1984
Db	7600	CCCCGGGAAGACCTGGGAATGGT---CAGGCACTCGGATCTTGACATCCACATCGAGGGC	7656
Qy	1985	CTGATGGAGGGAAGGGG-----CTTGAACAGGGCCTCAGGGGAGCAGAGGGAG-----	2032
Db	7657	TGAAGGAGGGAGAGGGTTTGGTATCATGAGCAGAGCCTCAGGGTAGCAGAGGGAGGACCC	7716
Qy	2033	-GGCCCTACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCC-----TAGGAC	2082
Db	7717	TGGCCCTCCTGGGAGATGAGGAAGGCCTCAGGAGACCCAGCACCCCAAGGCAGGGAGCCC	7776
Qy	2083	ACCGCACCCCTGTCTGAGACTGAG--GCTGCCACTTCTGGCCTCAAGAATCAGAACGATG	2140
Db	7777	ACCCACCCCTGTCTGAGAATGAGGTGCCTCCTCTTTTAGCCTCAGGAATCCAAGGGATG	7836
Qy	2141	GGGACTCAGATTGCAT--GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAG	2198
Db	7837	GCAACTCAGGTCAGCAGAGGGGTGGGTCCAAGCCCTTCCAGGATCAAGGAAAGGAAGAC	7896
Qy	2199	GAGGGAGGACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTC	2258
Db	7897	GAGGGAGGATTCAGGGGGCCTTGCAATCCAGATCAGTGGAGACCTGGGCCCTGGGAGGTC	7956
Qy	2259	CAGGGCACGGTGGCCACATATGGCCCATATTTCTGCATCTTTGAGGT----GACAGGAC	2311

Db	7957	CTGGGCAAGGTAGCCACCTGTAGCTCATACTTCCTGCATCTTCGAGGTCACAGAGAGGAG	8016
Qy	2315	AGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCAGGATCCAT	2374
Db	8017	AGGGCTATGGTCTGAGGGGTGGTACTTCAGGTCCGCAGAGGGAGGAGTCCCAGGATCTAC	8076
Qy	2375	ATGGCCCAAGATGTGCC-CCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGG	2433
Db	8077	AGGACCCAAGGTGTGCCACACTTCACGAGGAATGGGGATACCTGTGGCTCAGAAAGACGG	8136
Qy	2434	GACTCCACACAGTCTGGCTGTCCCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGG	2493
Db	8137	GACCCACAGAGTCTGGCTGTCCCCCTGTTCTTAGCTCAGGGGGGACCAGAGGAGGGATGG	8196
Qy	2494	CGGTATGTTCCATTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATG	2553
Db	8197	CCCTATGTGCCAATTTCACTTGTTCACAGGCAGGAAGTTGGGGAACCTTCAGGGAGATG	8256
Qy	2554	GGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCA	2613
Db	8257	AGGTTTTGGAGTAAAGGGGCAATGTTTGCTCATCTCAGGGGGTTGGGGGTTGAGGAAGGG	8316
Qy	2614	CAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCCA	2673
Db	8317	CAGGCCCTGTCAGGAGCAAACATGAGT-ACCCACAGGAGGCCATCAGAACCCTCACCCCA	8375
Qy	2674	GAACCAAAGGGTCTAGCCCTGGACACCTCACCCAG-----GATGTGGCTTCTTTTTTC	2725
Db	8376	GAACCAAAGGGTCTAGCCCTGGGCACCCACACAGGGGTGACAGGATGTGGCTCCTTCTC	8435
Qy	2726	ACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCTCATTCTCAGAGGGTGACTCAGGTCA	2785
Db	8436	ATTTCTGATTCCAGATCTCAGTGAGGTGAGGACCTTGTTCTCAGAGGGTGACTCAGGTCA	8495
Qy	2786	ACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGG	2845
Db	8496	CCACAGGGACCCCCATCTGGTCTACAGACACAGTGGTCCCAGGATCTGCCAAGAGTCCTG	8555
Qy	2846	GTGAGGAACATGAGGGAGGACTGAGGGTACCCAGGACCAGAACACTGAGGGAGACTGCA	2905
Db	8556	GTGAGGAATGTGAGGGAGGATTGAGGGTACCACAGGGCCAGAACGCAGATGATGACCCCA	8615
Qy	2906	CAGAAATCAGCCCTGCCCCTGCTGTACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAG	2965
Db	8616	CAGAAATCAGCCCTGCTCCTGTTGTACCCCAGAGAGCATGGGCTTGGCTTTCTGCTGAG	8675
Qy	2966	GTCCTTCCGTTATCCTGGGATCATTGATGTACGGGACGGGGAGGCCCTTGGTCTGAGAAGG	3025
Db	8676	GTCCCTCTCTTATCCTGGGATCACTGGTGTACGGAGTGGGAGGCCCTTGGTCTGAGGGGG	8735
Qy	3026	CTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCA	3085
Db	8736	CTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGGCTCTGCCAGGAGTTGAGGTGAGGACCA	8795
Qy	3086	AGCGGGCACCTCACCCAGGACACATTAATTCCAATGAATTTGATATCTCTTGCTGCCCT	3145
Db	8796	AGCAGGCTCCGCATCCAGGACACATGGGTTCGAATTCGACATCTTTTGCTGTCTGT	8855
Qy	3146	TC-CCCAAGGACCTAGGCACGTGTGGCCAGATGTTTGTCCCTCCTGTCTTCCATTCCCT	3204

Db	8856	TCTTCGGAAGACCTAGGCACAGGTGGCCAGATGTGGGGTTTCTTAGGTCCT---	GTTCCC	8912
Qy	3205	TATCATGGATGTGAACTCTTGATTTGGATTTCCTCAGACCAGCAAAAGGGCAGGATCCAGG		3264
Db	8913	TCTCAGGCATGTGAGCTCTTGATCTGAGTTTCTCAGGCCAGCAAAAGAGTGGGATCCAGG		8972
Qy	3265	CCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGA		3324
Db	8973	CCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCCACTCCATGA		9032
Qy	3325	GAGTGGGGATGTTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGCCAGGGCTGT		3384
Db	9033	GAGTGGGGACCTCACAGAGTCCAGCCTACCCTCTTGATGGCACTGAGGGACCGGGGCTGT		9092
Qy	3385	GCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTTCCTCTTCCTGGAGCTCCAGGAACCAGG		3444
Db	9093	GCTTACAGTCTGCACCCTAAGGGCCCATGGATTTCCTCTCTAGGAGCTCCAGGAACAAGG		9152
Qy	3445	CAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTG		3504
Db	9153	CAGTGAGGCCTTGGTCTGAGACAGTGTCTCAGGTTACAGAGCAGAGGATGCACAGGCTG		9212
Qy	3505	TGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACA		3564
Db	9213	TGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAAGACACA		9272
Qy	3565	TAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAATCGACCTCTG		3624
Db	9273	TAGGACTCCAAAGAGTCTGGCCTCACCTCCCTACCATCAATCTGCAGAATCGACCTCTG		9332
Qy	3625	CTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTTCAGGTTTTTCAGGGGACAGG		3683
Db	9333	CTGGCCGGCTATACCCTGAGGTGCTCTCACTTCCTCCTTCAGGTTCTGAGCAGACAGG		9392
Qy	3684	CCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA		3743
Db	9393	CCAACCG-GAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA		9451
Qy	3744	AGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCC		3803
Db	9452	AGTAAGCCTTTGTTAGAGCCTCTAAGATTTGGTTCTCAGCTGAGGTCTCTCACATGCTCC		9511
Qy	3804	CTCTCTCCCGAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTG		3863
Db	9512	CTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCCAGCTTTTGCCCTGCACCTCTGCCTGCTG		9571
Qy	3864	CCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAG		3923
Db	9572	CCCTGACCAGAGTCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAG		9631
Qy	3924	CCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC-----		3975
Db	9632	GCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGGTGGGTGCACAGGCTCCTACTACTGAGG		9691
Qy	3976	-----CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGC		4019
Db	9692	AGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTCTGGTCCTGGCACCCTGGAGGAAGTGC		9751
Qy	4020	CCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTA		4079
Db	9752	CTGCTGCTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCCACTA		9811

Qy	4080	CCATCAACTTCACTCGACAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGG	4139
Db	9812		9871
Qy	4140	GGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGG	4199
Db	9872		9931
Qy	4200	CTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAG	4259
Db	9932		9991
Qy	4260	AAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAG	4319
Db	9992		10051
Qy	4320	CCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCC	4379
Db	10052		10111
Qy	4380	ACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATC	4439
Db	10112		10171
Qy	4440	AGATCATGCCCAAGACAGGCTTCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCG	4499
Db	10172		10231
Qy	4500	GCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGA	4559
Db	10232		10291
Qy	4560	GGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAA	4619
Db	10292		10351
Qy	4620	AGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGG	4678
Db	10352		10411
Qy	4679	GTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCA	4738
Db	10412		10471
Qy	4739	GTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAG	4798
Db	10472		10531
Qy	4799	AGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG----GGACTGGGCCAGTG	4854
Db	10532		10591
Qy	4855	CACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTT	4914
Db	10592		10649
Qy	4915	CACCTC----TGAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGA	4970
Db	10650		10709

Qy	4971	CTTGGAGATTATCTTTGTTCTCTTTTGGAAATGTTCAAATGTTTTTTTTTAAGGGATGG	5030
Db	10710	CTTGGAGATTATCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTTAATGGATGG	10768
Qy	5031	TTGAATGAACCTTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATAT	5090
Db	10769	TTGAATTAACCTTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATAT	10828
Qy	5091	AGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAA	5150
Db	10829	AGTTTAGGAGTAAGAGTCTTGTTTTTTATTTCAGATTGGGAAATCCGTTCTATTTGTGAA	10888
Qy	5151	TTGGG---ATAATAACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAA	5207
Db	10889	TTTGGGACATAATAACAGCAGTGAGTAAGTATTTAGAAGTGTG---AATTCACCGTGAA	10945
Qy	5208	ATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAG	5267
Db	10946	ATAGGTGAGAT-----AAATTAAGATACTTAATTCCCGCCTTATGCCCTCAG	10993
Qy	5268	TCTATTCTGTAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGA	5327
Db	10994	TCTATTCTGTAAAATTTAAAAATATATATGCATACCTGGATTTCCTTGGCTTC---GTGA	11050
Qy	5328	ATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTC	5387
Db	11051	ATGTAAGAGAAATTAAATCTGAATAAATAATTCTTTCTGTAACTGGCTCATTTCTTCTC	11110
Qy	5388	CATGCACTGAGCATCTGCTTTTTTGAAGGCCCTGGGTAGTAGTGAGATGCTAAGGTAA	5447
Db	11111	TATGCACTGAGCATCTGCTCTGTGGAAGGCCAGGATTAGTAGTGAGATACAGGGTAA	11170
Qy	5448	GCCAGACTCATACCCACCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAG	5507
Db	11171	GCCAGACACACACTACCGATAGGGTATTAAGAGTCTAGGAGCGCGGTCATATAATTAAAG	11230
Qy	5508	GTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCT	5567
Db	11231	GTGACAAGATGTCCTCTAAGATGTAGGGGAAAAGT----AACGAGTGTGGGTATGGGGCT	11286
Qy	5568	CCGGGTGAGAGTGGTGGAGTGTCATGCCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAAC	5627
Db	11287	CCAGGTGAGAGTGGTGGGTGTAAATCCCTGTG-TGGGGCCTTTTGGGCTTTGGGAAAC	11345
Qy	5628	TGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674
Db	11346	TGCATTTTCTTCTGAGGGATCTGATTCTAATGAAGCTTGGTGGGTCC	11392

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e- 8.rst.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-8.rst.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 10:02:12 ; Search time 24214 Seconds
(without alignments)
13103.423 Million cell updates/sec

Title: US-08-819-669E-8
Perfect score: 5674
Sequence: 1 CCCGGGGCACCCTGGCATC.....TAATGATCTGGGTGGATCC 5674

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gss1:*
12: gb_gss2:*
13: gb_gss3:*
14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1062	18.7	1652	6	CR594285	CR594285 full-leng
2	1036.4	18.3	2151	6	HSM806642	BX640600 Homo sapi
3	1034.4	18.2	1671	6	CR622709	CR622709 full-leng
4	1032	18.2	1689	6	CR595748	CR595748 full-leng
5	1022.4	18.0	1738	6	CR623041	CR623041 full-leng
6	1008.6	17.8	1661	6	CR611124	CR611124 full-leng
7	918	16.2	930	14	DQ034885	DQ034885 Homo sapi
8	840.2	14.8	1020	2	BM459064	BM459064 AGENCOURT
9	787.2	13.9	923	14	DQ034886	DQ034886 Pan trogl
10	783.6	13.8	1739	6	CR619399	CR619399 full-leng
11	740.2	13.0	909	3	BU157186	BU157186 AGENCOURT
c 12	720.2	12.7	747	4	CA428506	CA428506 UI-H-FE1-
13	700	12.3	954	14	DQ049942	DQ049942 Homo sapi
14	678.4	12.0	1008	14	DQ034795	DQ034795 Homo sapi
15	675.8	11.9	811	3	BQ224380	BQ224380 AGENCOURT
16	652	11.5	937	3	BU153093	BU153093 AGENCOURT
c 17	645	11.4	668	4	CA423766	CA423766 UI-H-FE1-
18	621.4	11.0	623	8	CV023387	CV023387 311 Full
c 19	615.8	10.9	1044	1	AL562721	AL562721 AL562721
c 20	615	10.8	637	3	BM989182	BM989182 UI-H-DP0-
21	609	10.7	1191	3	BM907822	BM907822 AGENCOURT
c 22	607.6	10.7	1041	4	BX361005	BX361005 BX361005
23	602.6	10.6	957	14	DQ035556	DQ035556 Pan trogl
24	601	10.6	957	14	DQ035555	DQ035555 Homo sapi
25	583.8	10.3	918	14	DQ049943	DQ049943 Pan trogl
26	583	10.3	964	4	BX361006	BX361006 BX361006
27	566.6	10.0	922	3	BU175213	BU175213 AGENCOURT
28	562.4	9.9	947	4	BX384326	BX384326 BX384326
29	558.8	9.8	1006	14	DQ034796	DQ034796 Pan trogl
30	537.4	9.5	876	2	BF792356	BF792356 602252896
31	536.8	9.5	1021	2	BM470991	BM470991 AGENCOURT
32	532.2	9.4	960	14	DQ031722	DQ031722 Pan trogl
33	531	9.4	878	2	BG397171	BG397171 602434130
34	528.8	9.3	960	14	DQ031721	DQ031721 Homo sapi
35	526.6	9.3	1050	2	BG024106	BG024106 602303163
36	525.2	9.3	1016	3	BM556490	BM556490 AGENCOURT
37	524.6	9.2	1057	3	BM562570	BM562570 AGENCOURT
38	524.4	9.2	1049	4	CA488474	CA488474 AGENCOURT
39	523	9.2	1002	3	BM562465	BM562465 AGENCOURT
40	522.6	9.2	802	14	DQ034776	DQ034776 Homo sapi
41	522.6	9.2	962	2	BG116297	BG116297 602318570
42	522.4	9.2	1011	4	BX341218	BX341218 BX341218
43	520.8	9.2	872	2	BM449726	BM449726 AGENCOURT
44	519.4	9.2	806	2	BG030623	BG030623 602299402
45	516.4	9.1	1066	2	BM549169	BM549169 AGENCOURT

ALIGNMENTS

RESULT 1
CR594285
LOCUS

CR594285

1652 bp

mRNA

linear

HTC 21-JUL-2004

Db	342	TCAGGGAGCCTCCACCCTCCCCACTACCATCAACTATACTCTCTGGAGTCAATCCGATGA	401
Qy	4114	GGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCCTTGT	4173
Db	402	GGGCTCCAGCAACGAAGAAGAGGAAGGGCCAAGCACCTTTCCTGACCTGGAGACGAGCTT	461
Qy	4174	CCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATATCG	4233
Db	462	CCAAGTAGCACTCAGTAGGAAGATGGCTGAGTTGGTTTCATTTCTGCTCCTCAAGTATCG	521
Qy	4234	AGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCA	4293
Db	522	AGCCAGGGAGCCATTACAAAGGCAGAAATGCTGGGGAGTGTATCAGAAATTTCCAGGA	581
Qy	4294	CTGTTTTCTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGA	4353
Db	582	CTTCTTTCTCTGTGATCTTCAGCAAAGCCTCCGAGTACTTGACGCTGGTCTTTGGCATCGA	641
Qy	4354	CGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTTGTCACCTGCCTAGGTCTCTC	4413
Db	642	GGTGGTGGAAAGTGGTCCGCATCGGCCACTTGTACATCCTTGTACCTGCCTGGGCCTCTC	701
Qy	4414	CTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGT	4473
Db	702	CTACGATGGCCTGCTGGGCGACAATCAGATCGTGCCCAAGACAGGCTTCCTGATAATCGT	761
Qy	4474	CCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCT	4533
Db	762	CCTGGCCATAATCGCAAAAGAGGGCGACTGTGCCCTGAGGAGAAAATCTGGGAGGAGCT	821
Qy	4534	GAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCT	4593
Db	822	GAGTGTGTTGGAGGCATCTGATGGGAGGGAGGACAGTGTCTTTGCGCATCCAGGAAGCT	881
Qy	4594	GCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGA	4652
Db	882	GCTCACCCAAGATTTGGTGCAGGAAAAC TACCTGGAGTACCGGCAGTCCCCGGCAGTGA	941
Qy	4653	TCCCGCACGCTATGAGTTCTGTGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAA	4712
Db	942	TCCTGCATGCTACGAGTTCTGTGGGTCCAAGGGCCCTCGTTGAAACCAGCTATGTGAA	1001
Qy	4713	AGTCCTTGAGTATGTGATCAAGGTCAAGTGCAGAGTTTCGCTTTTTCTTCCCATCCCTGCG	4772
Db	1002	AGTCCTGCACCATTGCTAAAGATCAGTGGAGGACCTCACATTTCTACCCACCCCTGCA	1061
Qy	4773	TGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAG	4832
Db	1062	TGAATGGGCTTTTAGAGAGGGGGAAGAGTGAGTCTGAGCACGAGTTGCAGCCAGGGCCAG	1121
Qy	4833	TGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCCTC	4892
Db	1122	TGGGAGGGGGTCTGGGCCAGTGCACCTTCCAAGGCCCCATCCATTAGTTTCCACTGCCTC	1181
Qy	4893	GTGTGACATGAGGCCATTCTTCACTC--TGAAGAGAGCGGTGAGTGTCTCAGTAGTAG	4950
Db	1182	GTGTGATATGAGGCCATTCTTCACTCTTTGAAGAGAGCAGTCAGTATTGTTAGTAGTGA	1241
Qy	4951	GTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAAA	5010
Db	1242	GTTTCTGTTCTATTGGATGACTTTGAGATTTATCTTTGTTTCTGTTGGGAATTGTTCAAA	1301

Qy	5011	TGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATGACAGCAG	5070
Db	1302	TGTTCC-TTTTAACGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATGACAGTAG	1360
Qy	5071	TCACAC--AGTTCGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGG	5128
Db	1361	TCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTGTGTTTTTTATTTCAGATTGG	1420
Qy	5129	GAAATCCATTCTATTTTGTGAATTGGGA-TAATAACAGCAGTGGAAATAAGTA----CTTA	5183
Db	1421	GAAATCCATTCCATTTTGTGAATTGTGACAAATAACAGCAGTGGAAAAAGTATGTGCTTA	1480
Qy	5184	GAAATGTGAAA-AATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGAT	5242
Db	1481	GAATTGTGAAAGAATTAGCAGTAAAATACATGAGATAAAGACCTCAAGAAGTTAAAGAT	1540
Qy	5243	AGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGCATAC	5302
Db	1541	ACTTAATTCTTGCCTTATACCTCACTCTATTCTGTAAATTTGAAAAAAAAGCATGGATAC	1600
Qy	5303	CTGGATTTCCTTGGCTTCTTTTGAGAATGTAAGAGAAATTAATCTGAATAAA	5354
Db	1601	CTGGATATCCTTGGCTTCTTTTGAGAATTTAAGAGAAATTAATCTGAATAAA	1652

```

/db_xref="taxon:9606"
/clone="DKFZp686A13192"
/tissue_type="esophagus tumor"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
/note="melanoma antigen, family A, 6"
gene      1. .2151
          /gene="DKFZp686A13192"
CDS       569. .1513
          /gene="DKFZp686A13192"
          /codon_start=1
          /product="hypothetical protein"
          /protein_id="CAE45706.1"
          /db_xref="GI:34364601"
          /db_xref="InterPro:IPR002190"
          /translation="MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSST
LVEVTLGEVPAAESPDPQPQSPQGASSLPTTMNYPLWSQSYEDSSNQEEEGPSTFPDLE
SEFQAALSRKVAKLHVHLLKLRAREPVTKAEMLGSVVGNWQYFFPVIFSKASDSLQL
VFGIELMEVDPIGHVYIFATCLGLSYDGLLDNQIMPKTGFLIIILAIIAKEGDCAPE
EKIWEELSVLEVFEGREDSIFGDPKLLTQYFVQENYLEYRQVPGSDPACYEFLWGPR
ALIETSYVKVLHHMVKISGGPRISYPLLHEWALREGE"

```

ORIGIN

Query Match 18.3%; Score 1036.4; DB 6; Length 2151;
 Best Local Similarity 82.1%; Pred. No. 1.8e-247;
 Matches 1300; Conservative 0; Mismatches 251; Indels 33; Gaps 8;

```

Qy      3816 GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACCAGAG 3875
          ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      504 GCCAGTGGGTCTCCATTGCCCAGCTCCTGCCCACACTCCCGCCTGTTGCCCTGACCAGAG 563

Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      564 TCATCATGCCTCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCCTTGAGGCCC 623

Qy      3936 AACAGAGGCCCTGGGCCCTGGTGTGTGTGCAGGCT-----GCCA 3974
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      624 GAGGAGAGGCCCTGGGCCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGGCTG 683

Qy      3975 CCTCCTCCTCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAA 4034
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      684 CCTCCTCCTCTCTACTCTAGTTGAAGTCACCCTGGGGGAGGTGCCTGCTGCCGAGTCAC 743

Qy      4035 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTC 4094
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      744 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCCACTACCATGAACCTACCTC 803

Qy      4095 GACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTT 4154
          ||| ||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      804 TCTGGAGCCAATCCTATGAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCC 863

Qy      4155 GTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTT 4214
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      864 CTGACCTGGAGTCTGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCAAGTTGGTTCATT 923

Qy      4215 TTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTG 4274
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      924 TTCTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTG 983

Qy      4275 TCATCAAAAATTACAAGCACTGTTTCTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGC 4334

```

Db	984	TCGTCGGAAATTGGCAGTACTTCTTTCTGTGATCTTCAGCAAAGCTTCCGATTCTTGC	1043
Qy	4335	AGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGCCACTCCTATGTCTTG	4394
Db	1044	AGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTG	1103
Qy	4395	TCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCAAGA	4454
Db	1104	CCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCAAGA	1163
Qy	4455	CAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGG	4514
Db	1164	CAGGCTTCCTGATAATCATCCTGGCCATAATCGCAAAGAGGGCGACTGTGCCCTGAGG	1223
Qy	4515	AGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCT	4574
Db	1224	AGAAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGGAGGGAGGGAAGACAGTATCT	1283
Qy	4575	ATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-C	4633
Db	1284	TCGGGGATCCCAAGAAGCTGCTCACCCAATATTCGTGCAGGAAAACCTACCTGGAGTACC	1343
Qy	4634	GGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCG	4693
Db	1344	GGCAGGTCCCCGGCAGTGATCCTGCATGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCA	1403
Qy	4694	CTGAAACCAGCTATGTGAAAGTCCCTTGAGTATGTGATCAAGGTCAGTCAAGAGTTCGCT	4753
Db	1404	TTGAAACCAGCTATGTGAAAGTCCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCGCA	1463
Qy	4754	TTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCAT	4813
Db	1464	TTTCTTACCCACTCCTGCATGAGTGGGCTTTGAGAGAGGGGAAGAGTGAGTCTGAGCAC	1523
Qy	4814	GAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTC	4873
Db	1524	GAGTTGCAGCCAGGGCCAGTGGGAGGGGGTTTGGGCCAGTGCACCTTCCGGGGCCCATC	1583
Qy	4874	CAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCTCACCTC--TGAAGAGAGCGG	4931
Db	1584	CCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCCATCTTCTCACCTCTTTGAAGCGAGCAG	1643
Qy	4932	TCAGTGTTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTC	4991
Db	1644	TCAGCATTCTTAGTAGTGGGTTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTT	1703
Qy	4992	TCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCA	5051
Db	1704	CCTGTTGGAGTTGTTCAAATG-TTCCTTTTAACGGATGGTTGAATGAGCGTCAGCATCCA	1762
Qy	5052	AGTTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCT	5109
Db	1763	GGTTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCT	1822
Qy	5110	TGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAGCA	5167
Db	1823	TGTTTTTTATTTCAGATTGGGAAATCCATTCCATTTTGTGAATTGTGACATAATAATAGCA	1882
Qy	5168	GTGGAATAAGTACTT-AGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACT	5226

Db	1883	GTGGAAAAAGTATTTGCTTAAATTGTGAGCGAATTAGCAATAACATACATGAGATAACT	1942
Qy	5227	AAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTT	5286
Db	1943	CAAGAAATCAAAGATAGTTGATTCTTGCCCTGTACCTCAATCTATTCTGTAAAA---TT	1999
Qy	5287	AAAGATATATGCATACCTGGATTTTCCTTGGCCCTCTTTGAGAATGTAAGAGAAATTTAAATC	5346
Db	2000	AAACAAATATGCAACCAGGATTTTCCTTGACTTCTTTGAGAATGCAAGCGAAATTTAAATC	2059
Qy	5347	TGAATAAAGAATTCTTCCTGTTCA	5370
Db	2060	TGAATAAATAATTCTTCCTCCTTCA	2083

```

Db      119 GCCTGTGGGTCCCCATTGCCAGCTTTTGCCTGCACTCTTGCTGCTGCCCTGACCAGAG 178
Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935
Db      179 TCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCC 238
Qy      3936 AACAAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC----- 3975
Db      239 AAGAAGAGGCCCTGGGCCTGGTGGGTGCACAGGCTCCTACTACTGAGGAGCAGGAGGCTG 298
Qy      3976 ----CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTGGAGGAGGTGCCCACTGCTGGGT 4031
Db      299 CTGTCTCCTCCTCCTCTCCTCTGGTCCTGGCACCTGGAGGAAGTGCTGCTGAGT 358
Qy      4032 CAACAGATCCTCCCCAGAGTCTCAGGGAGCCTCCGCCTTTCCTACTACCATCAACTTCA 4091
Db      359 CAGCAGGTCTCCCCAGAGTCTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCA 418
Qy      4092 CTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCT 4151
Db      419 CTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCT 478
Qy      4152 CTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTGTTG 4211
Db      479 CGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTC 538
Qy      4212 GTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGA 4271
Db      539 ATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGA 598
Qy      4272 GTGTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCT 4331
Db      599 GAGTCATCAAAAATTACAAGCGCTGCTTTCTGTGATCTTCGGCAAAGCCTCCGAGTCCC 658
Qy      4332 TGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCC 4391
Db      659 TGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCGCCAGCAACACCTACACC 718
Qy      4392 TTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCA 4451
Db      719 TTGTCACCTGCCTGGGCCCTTTCTCCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCA 778
Qy      4452 AGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTG 4511
Db      779 AGACAGGCCCTTCTGATAATCGTCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTG 838
Qy      4512 AGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTG 4571
Db      839 AGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTG 898
Qy      4572 CCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGT 4631
Db      899 TCTATGGGGAGCCCAGGAAACTGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGT 958
Qy      4632 A-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCC 4690
Db      959 ACCGGCAGGTACCGGCAGTAATCCTGCGCGCTATGAGTTCTGTGGGGTCCAAGGGCTC 1018
Qy      4691 TCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTC 4750

```

```

Db      1019 TGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTC 1078
Qy      4751 GCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAG 4810
      || || || |||||
Db      1079 GCATTGCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAG 1138
Qy      4811 CATGAGTTGCAGCCAAGGCCAGTGGGAGGG----GGACTGGGCCAGTGCACCTTCCAGGG 4866
      ||||| ||| ||| || ||||| || |||
Db      1139 CATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--G 1196
Qy      4867 CCGCGTCCAGCAGCTTCCCTGCGTCGTGTGACATGAGGCCCATTCCTTCACTC----TGA 4922
      || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1197 CCCTGTGCAGCAGCTTCCCTTGCCTCGTGTAAACATGAGGCCCATTCCTTCACTCTGTTTGA 1256
Qy      4923 AGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTA 4982
      ||| | ||||| ||||| ||||| || || ||||| ||||| |||||
Db      1257 AGAAAATAGTCAGTGTCTTAGTAGTGGGTTTCTATTTTGTGGATGACTTGGAGATTTA 1316
Qy      4983 TCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTT 5042
      ||| |||| |||| ||||| ||||| || || ||||| ||||| |||||
Db      1317 TCTCTGTTTCCTTTTACAATTGTTGAAATG--TTCCTTTAATGGATGGTTGAATTAACCTT 1375
Qy      5043 CAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTA 5102
      ||||| ||||| ||||| || || | || ||||| ||||| |||||
Db      1376 CAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTA 1435
Qy      5103 AGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCATTTTGTGAATTGGG---ATAA 5159
      ||||| ||||| ||||| ||||| ||||| ||||| || || |||||
Db      1436 AGAGTCTTGTTTTTTATTTCAGATTGGGAAATCCGTTCTATTTTGTGAATTGGGACATAA 1495
Qy      5160 TAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATA 5219
      ||||| ||||| ||||| |||| ||| || | ||||| |||||
Db      1496 TAACAGCAGTGGAGTAAGTATTTAGAAGTGTG---AATTCACCGTGAAATAGGTGAGAT- 1551
Qy      5220 AAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAA 5279
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1552 -----AAATTAAGATACTTAATTCCCGCCTTATGCCTCAGTCTATTCTGTAA 1600
Qy      5280 AATTT-TTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAA 5338
      ||||| ||| ||||| ||||| ||||| ||||| || ||||| |||||
Db      1601 AATTTAAAAAATATATATGCATACCTGGATTTCCTTGGCTTC---GTGAATGTAAGAGAA 1657
Qy      5339 ATTAAATCTGAATA 5352
      ||||| |||||
Db      1658 ATTAAATCTGAATA 1671

```

RESULT 4

CR595748

LOCUS CR595748 1689 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CS0DK007YN24 of HeLa cells Cot 25-normalized of Homo sapiens (human).

ACCESSION CR595748

VERSION CR595748.1 GI:50476555

KEYWORDS HTC; CNSLT_cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1689)

AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
REFERENCE	2 (bases 1 to 1689)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES	Location/Qualifiers
source	1. .1689 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DK007YN24" /tissue_type="HeLa cells Cot 25-normalized" /plasmid="pCMVSPORT_6"
ORIGIN	

Db 536 TTCTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTG 595

Qy 4275 TCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGC 4334
 || || ||||| || ||| ||||| ||||| ||||| || || |||||

Db 596 TCGTCGGAAATTGGCAGTACTTCTTTCTGTGATCTTCAGCAAAGCTTCCGATTCTTGC 655

Qy 4335 AGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTG 4394
 ||||| ||||| || ||| ||||| ||||| ||||| || || |||

Db 656 AGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTGC 715

Qy 4395 TCACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCAGATCATGCCCAAGA 4454
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 716 CCACCTGCCTGGGCCTCTCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCCAAGA 775

Qy 4455 CAGGCTTCCTGATAAATGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGG 4514
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 776 CAGGCTTCCTGATAATCATCCTGGCCATAATCGCAAAGAGGGCGACTGTGCCCTGAGG 835

Qy 4515 AGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCT 4574
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Db 836 AGAAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGAAGACAGTATCT 895

Qy 4575 ATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-C 4633
 |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||

Db 896 TCGGGGATCCCAAGAAGCTGCTCACCCAATATTTCTGTCAGGAAAACCTACCTGGAGTACC 955

Qy 4634 GGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCG 4693
 ||||| || || ||||| ||||| ||||| ||||| ||||| |||||

Db 956 GGCAGGTCCCCGGCAGTGATCCTGCATGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCA 1015

Qy 4694 CTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCT 4753
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1016 TTGAAACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCGCA 1075

Qy 4754 TTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCAT 4813
 |||| |||| |||| |||| ||||| ||||| ||||| ||||| |||||

Db 1076 TTTCTTACCACTCCTGCATGAGTGGGCTTTGAGAGAGGGGAAGAGTGAAGTCTGAGCAC 1135

Qy 4814 GAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTC 4873
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1136 GAGTTGCAGCCAGGGCAGTGGGAGGGGGTTTGGGCCAGTGCACCTTCCGGGGCCCCATC 1195

Qy 4874 CAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTC--TGAAGAGAGCGG 4931
 | || |||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1196 CCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCATTCTTCACTCTTTGAAGCGAGCAG 1255

Qy 4932 TCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTT 4991
 |||| |||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1256 TCAGCATTCTTAGTAGTGGGTTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTT 1315

Qy 4992 TCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCA 5051
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1316 CCTGTTGGAGTTGTTCAAATG-TTCCTTTTAACGGATGGTTGAATGAGCGTCAGCATCCA 1374

Qy 5052 AGTTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCT 5109
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1375 GGTTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCT 1434

Qy 5110 TGTGTTTTTATTGAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAGCA 5167
 ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1435 TGTTTTTTTATTGAGATTGGGAAATCCATTCCATTTTGTGAATTGTGACATAATAATAGCA 1494

Qy	5168	GTGGAATAAGTACTT-AGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACT	5226
Db	1495	GTGGAATAAGTATTTGCTTAAATTTGTGAGCGAATTAGCAATAACATACATGAGATAACT	1554
Qy	5227	AAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTT	5286
Db	1555	CAAGAAATCAAAGATAGTTGATTCTTGCCCTGTACCTCAATCTATTCTGTAAAA---TT	1611
Qy	5287	AAAGATATATGCATACCTGGATTTCTTGCCCTCTTTGAGAATGTAAGAGAAATTAAATC	5346
Db	1612	AAACAAATATGCAACCAGGATTTCTTGACTTCTTTGAGAATGCAAGCGAAATTAAATC	1671
Qy	5347	TGAATAAAGAATTCTTCC	5364
Db	1672	TGAATAAATAATTCTTCC	1689

Matches 1308; Conservative 0; Mismatches 196; Indels 58; Gaps 11;

```
Qy      3816 GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875
          |||||
Db      198 GCCTGTGGGTCCCCATTGCCCAGCTTTTGCCTGCACTCTTGCCCTGCTGCCCTGACCAGAG 257

Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935
          |||||
Db      258 TCATCATGTCTCTTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCC 317

Qy      3936 AACAAAGAGGCCCTGGGCTGGTGTGTGTGCAGGCTGCCAC----- 3975
          |||||
Db      318 AAGAAGAGGCCCTGGGCTGGTGGGTGCACAGGCTCCTACTACTGAGGAGCAGGAGGCTG 377

Qy      3976 ----CTCCTCCTCCTCCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGT 4031
          |||||
Db      378 CTGTCTCCTCCTCCTCCTCCTCTGGTCCCTGGCACCCTGGAGGAAGTGCTGCTGCTGAGT 437

Qy      4032 CAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCA 4091
          |||||
Db      438 CAGCAGGTCTCCTCCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCA 497

Qy      4092 CTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGGCCAAGCACCT 4151
          |||||
Db      498 CTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGGCCAAGCACCT 557

Qy      4152 CTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTG 4211
          |||||
Db      558 CGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTC 617

Qy      4212 GTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGA 4271
          |||||
Db      618 ATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGA 677

Qy      4272 GTGTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCT 4331
          |||||
Db      678 GAGTCATCAAAAATTACAAGCGCTGCTTTCTGTGATCTTCGGCAAAGCCTCCGAGTCCC 737

Qy      4332 TGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCC 4391
          |||||
Db      738 TGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCGCCAGCAACACCTACACCC 797

Qy      4392 TTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCA 4451
          |||||
Db      798 TTGTCACCTGCCTGGGCCCTTCCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCA 857

Qy      4452 AGACAGGCTTCCTGATAAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTG 4511
          |||||
Db      858 AGACAGGCCTTCTGATAATCGTCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTG 917

Qy      4512 AGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTG 4571
          |||||
Db      918 AGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTG 977

Qy      4572 CCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGT 4631
          |||||
Db      978 TCTATGGGGAGCCCAGGAACTGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGT 1037

Qy      4632 A-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCC 4690
          |||||
Db      1038 ACCGGCAGGTACCGGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTC 1097
```

Qy	4691	TCGCTGAAACACAGCTATGTGAAAAGTCCTTGAGTATGTGATCAAGGTCAGTGC AAGAGTTC	4750
Db	1098	TGGCTGAAACACAGCTATGTGAAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTC	1157
Qy	4751	GCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAG	4810
Db	1158	GCATTGCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAG	1217
Qy	4811	CATGAGTTGCAGCCAAGGCCAGTGGGAGGG----GGACTGGGCCAGTGCACCTTCCAGGG	4866
Db	1218	CATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--G	1275
Qy	4867	CCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTC----TGA	4922
Db	1276	CCCTGTGCAGCAGCTTCCCCTGCCTCGTGTAAACATGAGGCCCATTCCTTCACTCTGTTTGA	1335
Qy	4923	AGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCCTATTGGGTGACTTGGAGATTTA	4982
Db	1336	AGAAAATAGTCAGTGTCTTAGTAGTGGGTTTCTATTTTGTGGATGACTTGGAGATTTA	1395
Qy	4983	TCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTT	5042
Db	1396	TCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTTAATGGATGGTTGAATTAACCTT	1454
Qy	5043	CAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAAGGGTA	5102
Db	1455	CAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTA	1514
Qy	5103	AGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG---ATAA	5159
Db	1515	AGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCGTTCTATTTTGTGAATTTGGGACATAA	1574
Qy	5160	TAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATA	5219
Db	1575	TAACAGCAGTGGAGTAAGTATTTAGAAGTGTG---AATTCACCGTGAAATAGGTGAGAT-	1630
Qy	5220	AAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAA	5279
Db	1631	-----AAATTAAGATACTTAATCCCGCCTTATGCCTCAGTCTATTCTGTAA	1679
Qy	5280	AATTT-TTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAA	5338
Db	1680	AATTTAAAAATATATATGCATACCTGGATTTCCTTGGCTTC--GTGAATGTAAGAGAA	1736
Qy	5339	AT 5340	
Db	1737	AT 1738	

```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1  (bases 1 to 1661)
AUTHORS        Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE          Full-length cDNA libraries and normalization
JOURNAL        Unpublished
REMARK         Contact : Feng Liang Email : fliang@lifetech.com URL :
                http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                Faraday Avenue
REFERENCE      2  (bases 1 to 1661)
AUTHORS        Genoscope.
TITLE          Direct Submission
JOURNAL        Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT        1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
                end enriched, double-strand cDNA was digested with Not I and cloned
                into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
                was normalized. Library was constructed by Life Technologies, a
                division of Invitrogen.
FEATURES
    source      Location/Qualifiers
                1. .1661
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="CS0DC020YG12"
                /tissue_type="Neuroblastoma Cot 25-normalized"
                /plasmid="pCMVSPORT_6"
ORIGIN

```

Qy	4215	TTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTG	4274
Db	533	TTCTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTG	592
Qy	4275	TCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGC	4334
Db	593	TCGTCGGAAATTGGCAGTACTTCTTTCTGTGATCTTCAGCAAAGCTCCGATTCTTGC	652
Qy	4335	AGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTG	4394
Db	653	AGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCATCGGCCACGTGTACATCTTG	712
Qy	4395	TCACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCAGATCATGCCAAGA	4454
Db	713	CCACCTGCCTGGGCCTCTCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAAGA	772
Qy	4455	CAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGG	4514
Db	773	CAGGCTTCCTGATAATCATCCTGGCCATAATCGCAAAAGAGGGCGACTGTGCCCTGAGG	832
Qy	4515	AGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCT	4574
Db	833	AGAAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTTGAGGGGAGGGAAGACAGTATCT	892
Qy	4575	ATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-C	4633
Db	893	TCGGGGATCCCAAGAAGCTGCTCACCCAATATTTCTGTCAGGAAAAGTACCTGGAGTACC	952
Qy	4634	GGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCG	4693
Db	953	GGCAGGTCCCCGGCAGTGATCCTGCATGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCA	1012
Qy	4694	CTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGCT	4753
Db	1013	TTGAAACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCGCA	1072
Qy	4754	TTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCAT	4813
Db	1073	TTTCTTACCCACTCCTGCATGAGTGGGCTTTGAGAGAGGGGGAAGAGTGAGTCTGAGCAC	1132
Qy	4814	GAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTC	4873
Db	1133	GAGTTGCAGCCAGGGCCAGTGGGAGGGGGTTTGGGCCAGTGCACCTTCCGGGGCCCCATC	1192
Qy	4874	CAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCAC'--TGAAGAGAGCGG	4931
Db	1193	CCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCATTCTTCAC'TTTGAAGCGAGCAG	1252
Qy	4932	TCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTC	4991
Db	1253	TCAGCATTCTTAGTAGTGGGTTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTT	1312
Qy	4992	TCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC'TTCAGCATCCA	5051
Db	1313	CCTGTTGGAGTTGTTCAAATG-TTCCTTTTAACGGATGGTTGAATGAGCGTCAGCATCCA	1371
Qy	5052	AGTTTATGAATGACAGCAGTCACAC--AGTTCGTGTATATAGTTTAAGGGTAAGAGTCT	5109
Db	1372	GGTTTATGAATGACAGTAGTCACACATAGTGTGTTTATATAGTTTAGGAGTAAGAGTCT	1431

```

Qy      5110 TGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAGCA 5167
      ||| ||||||||||||||||||||||||||||||||||| ||| ||||| ||||
Db      1432 TGTTTTTTTATTTCAGATTGGGAAATCCATTCCATTTTGTGAATTGTGACATAATAATAGCA 1491

Qy      5168 GTGGAATAAGTACTT-AGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAAGT 5226
      ||||| ||||| || || | | | || | || | || |||
Db      1492 GTGGAAAAAGTATTTGCTTAAAATTGTGAGCGAATTAGCAATAACATACATGAGATAACT 1551

Qy      5227 AAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTT 5286
      ||||| || ||||| ||||||||||| ||||||| ||||||||||| ||
Db      1552 CAAGAAATCAAAAGATAGTTGATTCTTGCCTTGACCTCAATCTATTCTGTAAAA--TT 1608

Qy      5287 AAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAA 5339
      ||| | ||||| || ||||||||||| ||||||||||| ||| ||||
Db      1609 AAACAAATATGCAAACCAGGATTTCCTTGACTTCTTTGAGAATGCAAGCGAAA 1661

```

RESULT 7

DQ034885

LOCUS DQ034885 930 bp DNA linear GSS 02-JUN-2005

DEFINITION Homo sapiens MAGEA1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION DQ034885

VERSION DQ034885.1 GI:66886094

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 930)

AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees

JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)

PUBMED 15869325

REFERENCE 2 (bases 1 to 930)

AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.

FEATURES Location/Qualifiers

```

source      1..930
              /organism="Homo sapiens"
              /mol_type="genomic DNA"
              /db_xref="taxon:9606"
              /chromosome="X"

gene        <1..>930
              /gene="MAGEA1"
              /locus_tag="HC4290"

```

ORIGIN

Query Match 16.2%; Score 918; DB 14; Length 930;
Best Local Similarity 99.9%; Pred. No. 6.6e-218;

Matches 929; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	3881	ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA	3940
Db	1	ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA	60
Qy	3941	GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTG	4000
Db	61	GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTG	120
Qy	4001	GGCACCCTGGAGGAGGTGCCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA	4060
Db	121	GGCACCCTGGAGGAGGTGCCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGA	180
Qy	4061	GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC	4120
Db	181	GCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCC	240
Qy	4121	AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCA	4180
Db	241	AGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCA	300
Qy	4181	GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG	4240
Db	301	GTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGG	360
Qy	4241	GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTT	4300
Db	361	GAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTT	420
Qy	4301	CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCACTGGTCTTTGGCATTGACGTGAAG	4360
Db	421	CCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCACTGGTCTTTGGCATTGACGTGAAG	480
Qy	4361	GAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGAT	4420
Db	481	GAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGAT	540
Qy	4421	GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGCTCTGGTC	4480
Db	541	GGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGCTCTGGTC	600
Qy	4481	ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG	4540
Db	601	ATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTG	660
Qy	4541	ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC	4600
Db	661	ATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACC	720
Qy	4601	CAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCA	4659
Db	721	CAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCA	780
Qy	4660	CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT	4719
Db	781	CGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTT	840
Qy	4720	GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA	4779
Db	841	GAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCA	900

Qy 4780 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGA 4809
 |||
 Db 901 GCTTTGAGAGAGGAGGAAGAGGGAGTCTGA 930

RESULT 8

BM459064

LOCUS BM459064 1020 bp mRNA linear EST 05-FEB-2002

DEFINITION AGENCOURT_6414460 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5557380
 5', mRNA sequence.

ACCESSION BM459064

VERSION BM459064.1 GI:18508104

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 1020)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM12278 row: k column: 13

High quality sequence stop: 605.

FEATURES

source

Location/Qualifiers

1..1020

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5557380"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_72"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN

Query Match 14.8%; Score 840.2; DB 2; Length 1020;

Best Local Similarity 97.8%; Pred. No. 2.1e-198;

Matches 870; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

Qy 4411 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 4470
 |||

Db 1 CTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAAT 60

Qy 4471 TGTCTTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA 4530
 |||

Db 61 TGTCTTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGA 120

Qy 4531 GCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAA 4590
 |||
 Db 121 GCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAA 180

Qy 4591 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAG 4649
 |||
 Db 181 GCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAG 240

Qy 4650 TGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGT 4709
 |||
 Db 241 TGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTTGCTGAAACCAGCTATGT 300

Qy 4710 GAAAGTCCTTGAGTATGTGATCAAGGTCAAGAGTTCGCTTTTTCTTCCCATCCCT 4769
 |||
 Db 301 GAAAGTCCTTGAGTATGTGATCAAGGTCAAGAGTTCGCTTTTTCTTCCCATCCCT 360

Qy 4770 GCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGC 4829
 |||
 Db 361 GCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGC 420

Qy 4830 CAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGC 4889
 |||
 Db 421 CAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGC 480

Qy 4890 CTCGTGTGACATGAGGCCCATTCCTTCACTCTGAAGAGAGCGGTCAAGTGTCTCAGTAGTA 4949
 |||
 Db 481 CTCGTGTGACATGAGGCCCATTCCTTCACTCTGAAGAGAGCGGTCAAGTGTCTCAGTAGTA 540

Qy 4950 GGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAA 5009
 |||
 Db 541 GGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAA 600

Qy 5010 ATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCA 5069
 |||
 Db 601 ATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCA 660

Qy 5070 GTCACACAGTTCTGTGTATATAGTTTAAAGGTAAGAGTCTTGTGTTTTATTTCAGATTGGG 5129
 |||
 Db 661 GTCACACAGTTCTGTGTATATAGTTTAAAGGTAAGAGTCTTGTGTTTTATTTCAGATTGNG 720

Qy 5130 AAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGAATAAGTACTTAGAAAATG 5189
 |||
 Db 721 AAATCCATTCTATTTTGTGAATTGGGAACATAACAGCAGTGAATAAGTACTTAGAAAATG 780

Qy 5190 TGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAAT 5249
 |||
 Db 781 TNGAAAAATGAGCANGTAAATAGATGAGATAAAGAACTANAGAAATTAAGAGATAGTCAAT 840

Qy 5250 TCTTGCC-TTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGC 5298
 |||
 Db 841 TCTTGCCTTTATACCTCCGCCTATTCTGTAAAATTTTTAAAGATATATGC 890

RESULT 9
 DQ034886

LOCUS DQ034886 923 bp DNA linear GSS 02-JUN-2005
 DEFINITION Pan troglodytes MAGEA1 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION DQ034886
 VERSION DQ034886.1 GI:66886095
 KEYWORDS GSS.

```

SOURCE      Pan troglodytes (chimpanzee)
ORGANISM    Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1 (bases 1 to 923)
AUTHORS     Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE       A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
JOURNAL      (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED       15869325
REFERENCE   2 (bases 1 to 923)
AUTHORS     Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE       Direct Submission
JOURNAL      Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment. Translation starts at the beginning of
            alignment.
FEATURES             Location/Qualifiers
     source             1..923
                        /organism="Pan troglodytes"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9598"
     gene               <1..>923
                        /gene="MAGEA1"
                        /locus_tag="HC4290"
ORIGIN

Query Match      13.9%; Score 787.2; DB 14; Length 923;
Best Local Similarity 87.0%; Pred. No. 3.8e-185;
Matches 803; Conservative 0; Mismatches 119; Indels 1; Gaps 1;

Qy      3884 TCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAG 3943
          |||||  |||||  | ||| |||||  ||| | ||
Db      1 TCTCTTGAGCANNNGGAGTCTGNNNTNCAAGNCTGAGGAAGCCCTTGAGGNCAANANAAG 60

Qy      3944 GCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTCTGGGC 4003
          |||||  |||||
Db      61 GCCCTGGGCCTGNTGTGTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 120

Qy      4004 ACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCC 4063
          |||||  |||||
Db      121 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 180

Qy      4064 TCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGC 4123
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      181 TCCGCCTTTCCCACTACCATCAACTTCACTCGCCAGAGGCAACCCATTGAGGGTTCCAGC 240

Qy      4124 AGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTA 4183
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      241 AGCCGTGAAGAGGAGGGGCCAAGCACCTCTCGTATCCTGGAGTCCTTGTTCCGAGCAGTA 300

Qy      4184 ATCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAG 4243
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      301 ATCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAG 360

```

Qy 4244 CCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAAATTACAAGCACTGTTTTCTCT 4303
 |||
 Db 361 CCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAAATTACAAGCACTGTTTTCTCT 420
 Qy 4304 GAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAA 4363
 | |||
 Db 421 GTGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGAGGTGAAGGAA 480
 Qy 4364 GCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGC 4423
 |||
 Db 481 GCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTACGATGGC 540
 Qy 4424 CTGCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATG 4483
 |||
 Db 541 CTGCTGGGAGATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATG 600
 Qy 4484 ATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATG 4543
 |||
 Db 601 ATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATG 660
 Qy 4544 GAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAA 4603
 |||
 Db 661 GAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAA 720
 Qy 4604 GATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGC 4662
 |||
 Db 721 GATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCACGC 780
 Qy 4663 TATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAG 4722
 |||
 Db 781 TATGAGTNNCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAANNCTTGAG 840
 Qy 4723 TATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCT 4782
 |||
 Db 841 TATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGANGNAGCT 900
 Qy 4783 TTGAGAGAGGAGGAAGAGGGAGT 4805
 |||
 Db 901 TTGAGAGAGGAGGAAGAGGGAGT 923

RESULT 10

CR619399

LOCUS CR619399 1739 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CS0DI079YD09 of Placenta Cot 25-normalized of Homo sapiens (human).

ACCESSION CR619399

VERSION CR619399.1 GI:50500206

KEYWORDS HTC; CNSLT_cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1739)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
 Faraday Avenue

Qy	4326	AGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCT	4385
Db	689		
Qy	4386	AGTGCATGCAGGTGATCTTTGGCATTGATGTGAAGGAAGTGGACCTGCCGGCCACTCCT	748
Db	749		
Qy	4446	ATGTCCTTGTACCTGCCTAGGTCCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCA	4445
Db	749		
Qy	4446	ACATCCTTGTACCTGCCTGGGCCTCTCCTATGATGGCCTGCTGGGTGATGATCAGAGTA	808
Db	809		
Qy	4506	TGCCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATG	4505
Db	809		
Qy	4506	CGCCCCAAGACCGGCTCCTGATAATCGTCCTGGGCATGATCTTAATGGAGGGCAGCCGCG	868
Db	869		
Qy	4566	CTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGC	4565
Db	869		
Qy	4566	CCCCGGAGGAGGCAATCTGGGAAGCATTGAGTGTGATGGGGCTGTATGATGGGAGGGAGC	928
Db	929		
Qy	4566	ACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACC	4625
Db	929		
Qy	4626	ACAGTGTCTATTGGAAGCTCAGGAAGCTGCTCACCCAAGAGTGGGTGCAGGAGAACTACC	988
Db	989		
Qy	4626	TGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAA	4684
Db	989		
Qy	4685	TGGAGTACCGCCAGGCGCCCGGCAGTGATCCTGTGCGCTACGAGTTCCTGTGGGGTCCAA	1048
Db	1049		
Qy	4685	GGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAA	4744
Db	1049		
Qy	4745	GGGCCCTTGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAA	4744
Db	1049		
Qy	4745	GAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAG	4804
Db	1109		
Qy	4745	GAGTTCGCATTTCCTACCCATCCCTGCATGAAGAGGCTTTGGGAGAGGAGAAA--GGAG	1165
Db	1109		
Qy	4805	TCTGAGCATGAGTTGCAGCCAAGGCCAGTGG-----GAGGGGGACTTGGGCCAGTG	4854
Db	1166		
Qy	4805	TTTGAGCAGGAGTTGCAGCTAGGGCCAGTGGGGCAGGTTGTGGGAGGGCCTTGGGCCAGTG	1225
Db	1166		
Qy	4855	CACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCCTT	4914
Db	1226		
Qy	4855	CACGTTCCAGGGCCACATCCACCACCTTTCCTGCTC--TGTTACATGAGGCCCATTCCTT	1282
Db	1226		
Qy	4915	CACCTC-----TGAAGAGAGCGGTGAGTGTCTCAGTAGTAG-----	4950
Db	1283		
Qy	4915	CACTCTGTGTTTGAAGAGAGCAGTCACAGTTCTCAGTAGTGGGAGCATGTTGGGTGTGA	1342
Db	1283		
Qy	4951	-----GTTTCTGTCTATTGGGTGACTTGGAGATTTATC	4984
Db	1343		
Qy	4985	GGGAACACAGTGTGGACCATCTCTCAGTTCCTGTCTATTGGGCGATTTGGAGGTTTATC	1402
Db	1343		
Qy	4985	TTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCA	5044
Db	1403		
Qy	4985	TTTGTTTCCTTTTGGGAATTGTTCAAATG-TTCCTTCTAATGGATGGTGTAAATGAACCTCA	1461
Db	1403		
Qy	5045	GCATCCAAGTTTATGAATGACAGCAGTCACAC--AGTTCGTGTATATAGTTTAAAGGGTA	5102
Db	1462		
Qy	5045	ACATTC-ATTTTATGTATGACAGTAGACAGACTTACTGCTTTTTATATAGTTTAGGAGTA	1520
Db	1462		
Qy	5103	AGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATA--AT	5160
Db	1521		
Qy	5103	AGAGTCTTGCTTTTCATTTATACTGGGAAACCCATGTTATTTCTTGAATTCAGACACTAC	1580
Db	1521		
Qy	5161	AACAGCAGTGGAATAAG---TACTTAGAAATGTGAA--AAATGAGCAGTAAAATAGATGA	5215
Db	1580		

```

      || ||||| ||| |||| | ||||| ||||| ||| ||||| ||||| ||||
Db      1581 AAGAGCAGAGGATTAAGGTTTTTTTAGAAATGTGAAACAACATAGCAGTAAAATACATGA 1640

Qy      5216 GATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTA 5259
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1641 GATAAAGACATAAAGAAATTAACAATAGTTAATTCTTGCCTTA 1684

```

RESULT 11

BU157186

LOCUS BU157186 909 bp mRNA linear EST 04-SEP-2002

DEFINITION AGENCOURT_7941457 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6011608
5', mRNA sequence.

ACCESSION BU157186

VERSION BU157186.1 GI:22670718

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 909)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM13201 row: i column: 17

High quality sequence start: 18

High quality sequence stop: 583.

FEATURES

source

Location/Qualifiers

1. .909

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6011608"

/tissue_type="large cell carcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_68"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.8 kb. Library constructed by Life
Technologies. "

ORIGIN

Query Match 13.0%; Score 740.2; DB 3; Length 909;

Best Local Similarity 97.0%; Pred. No. 2.2e-173;

Matches 765; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

Qy 3816 GCCTGTGGGTCTTCATTGCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875

Db 40 GCCTGTGGGTCTTCATTGCCAGCTCCTGCCCACACTCCTGCCTGTTGCCCTGACGAGAG 99

Qy 3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935

```

Db      100 TCATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCC 159
Qy      3936 AACAAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCACCTCCTCCTCCTCCTCTGG 3995
Db      160 AACAAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCGCCTCCTCCTCCTCCTCTGG 219
Qy      3996 TCCTGGGCACCCCTGGAGGAGGTGCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC 4055
Db      220 TCCTGGGCACCCCTGGAGGAGGTGCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC 279
Qy      4056 AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGG 4115
Db      280 AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGG 339
Qy      4116 GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCC 4175
Db      340 GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCC 399
Qy      4176 GAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTCTGCTCCTCAAATATCGAG 4235
Db      400 GAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTCTGCTCCTCAAATATCGAG 459
Qy      4236 CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCAATCAAAAATTACAAGCACT 4295
Db      460 CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTCAATCAAAAATTACAAGCACT 519
Qy      4296 GTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACG 4355
Db      520 GTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACG 579
Qy      4356 TGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCT 4415
Db      580 TGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCT 639
Qy      4416 ATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCC 4475
Db      640 ATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGTTTCTGATAATTGGCC 699
Qy      4476 TGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGA 4535
Db      700 TGGTCCTGATTGCAATGGAAGGGGGCCATGCTCCTGGAGAGGAAATCTGGGACGACCTGA 759
Qy      4536 GTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTG-CCTATGGGGAGCCCAGGAAGCTG 4594
Db      760 ATGTGATGGAGGTGTATGATGGGAAGGAGCCCAGGGCCCTATGGGGAGCCCAGAACTG 819
Qy      4595 CTCACCCAA 4603
Db      820 CTCCACCCA 828

```

RESULT 12
CA428506/c

LOCUS CA428506 747 bp mRNA linear EST 07-NOV-2002
DEFINITION UI-H-FE1-bez-g-10-0-UI.s1 NCI_CGAP_FE1 Homo sapiens cDNA clone
UI-H-FE1-bez-g-10-0-UI 3', mRNA sequence.
ACCESSION CA428506
VERSION CA428506.1 GI:24791232
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 747)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: James Martin
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES Location/Qualifiers

source 1..747
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FE1-bez-g-10-0-UI"
 /tissue_type="Cell lines"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI_CGAP_FE1"
 /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
 (Pharmacia) with a modified polylinker; Site_1: EcoR I;
 Site_2: Not I; NCI_CGAP_FE1 is a normalized cDNA library
 derived from a pool of mRNA obtained from 3 cell lines
 from grade II chondrosarcoma tissues. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand cDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an EcoR I
 adaptor, digested with Not I, and cloned directionally
 into pT7T3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 CGCTACGGAC. The cell lines were provided by Dr James
 Martin from the University of Iowa.
 TAG_TISSUE=Human grade 2 chondrosarcoma cell line pool
 TAG_LIB=UI-H-FE1
 TAG_SEQ=CGCTACGGAC"

ORIGIN

Query Match 12.7%; Score 720.2; DB 4; Length 747;
 Best Local Similarity 99.6%; Pred. No. 2.2e-168;
 Matches 722; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4633 CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTC 4692
 ||||| |

Db 737 CGGCAGTGCCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTC 678

QY 4693 GCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGC 4752
 |||||

Db 677 GCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGC 618

```

Qy      4753 TTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCA 4812
        |||
Db      617 TTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCA 558

Qy      4813 TGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGT 4872
        |||
Db      557 TGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGT 498

Qy      4873 CCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGT 4932
        |||
Db      497 CCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGT 438

Qy      4933 CAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCT 4992
        |||
Db      437 CAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCT 378

Qy      4993 CTTTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAA 5052
        |||
Db      377 CTTTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAA 318

Qy      5053 GTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGT 5112
        |||
Db      317 GTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGT 258

Qy      5113 GTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGA 5172
        |||
Db      257 GTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGA 198

Qy      5173 ATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAA 5232
        |||
Db      197 ATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAA 138

Qy      5233 ATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAATTTTTAAAGAT 5292
        |||
Db      137 ATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAATTTTTAAAGAT 78

Qy      5293 ATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATA 5352
        |||
Db      77 ATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATA 18

Qy      5353 AAGAA 5357
        ||||
Db      17 AAGAA 13

```

RESULT 13

DQ049942

LOCUS DQ049942 954 bp DNA linear GSS 02-JUN-2005

DEFINITION Homo sapiens MAGEA4 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION DQ049942

VERSION DQ049942.1 GI:66903141

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 954)

AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,

Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 954)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES Location/Qualifiers
source 1. .954
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
gene <1. .>954
/gene="MAGEA4"
/locus_tag="HC17937"

ORIGIN

Query Match 12.3%; Score 700; DB 14; Length 954;
Best Local Similarity 85.3%; Pred. No. 2.6e-163;
Matches 814; Conservative 0; Mismatches 115; Indels 25; Gaps 2;

```

Qy      3881 ATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAA 3940
        |||||  |||||||  ||||  |||||||||||||||||||  |  |||||||||  ||
Db      1  ATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAA 60

Qy      3941 GAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC-----C 3976
        ||||||||||||||||  |||  |||||  |  ||  |
Db      61 GAGGCCCTGGGCCTGGTGGGTGCACAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTC 120

Qy      3977 TCCTCCTCCTCTCCTCTGGTCCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACA 4036
        ||||||||||||||||||  ||||||||||||  ||||  |||||  ||||  ||
Db      121 TCCTCCTCCTCTCCTCTGGTCCCTGGCACCCTGGAGGAAGTGCTGCTGCTGAGTCAGCA 180

Qy      4037 GATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGA 4096
        |  ||||||||||||||||  ||||  |||||  |||||  |||||  |
Db      181 GGTCTCCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTTGC 240

Qy      4097 CAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGT 4156
        |||||||||  ||||||||||||||||  ||||||||||||||||  |
Db      241 TGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCT 300

Qy      4157 ATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTT 4216
        |  ||||||||||||||||  ||  ||  |||  |||  |||||  ||  ||||  |  ||||
Db      301 GACGCAGAGTCCTTGTTCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTT 360

Qy      4217 CTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTC 4276
        |||||  ||  |||||||||  ||||  |||||||||||||||||||  |||
Db      361 CTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTC 420

Qy      4277 ATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 4336
        ||||||||||||||||  ||  |||||  ||||||||||||||||  |||||  ||  ||

```

Db 421 ATCAAAAATTACAAGCGCTGCTTTCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAG 480

Qy 4337 CTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTC 4396
 || ||||| ||||| ||||| ||||| ||||| |||||

Db 481 ATGATCTTTGGCATTGACGTGAAGGAAGTGACCCCGCCAGCAACACCTACACCCTTGTC 540

Qy 4397 ACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACA 4456
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 541 ACCTGCCTGGGCCTTTCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCAAGACA 600

Qy 4457 GGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAG 4516
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 601 GGCTTCCTGATAATCGTCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAG 660

Qy 4517 GAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTAT 4576
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 661 GAAATCTGGGAGGAGCTGGGTGTGATGGGGTGTATGATGGGAGGGAGCACACTGTCTAT 720

Qy 4577 GGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGG 4635
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 721 GGGGAGCCCAGGAAACTGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTACCGG 780

Qy 4636 CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT 4695
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 781 CAGGTACCCGGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTCTGGCT 840

Qy 4696 GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT 4755
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 841 GAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATT 900

Qy 4756 TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGA 4809
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 901 GCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGA 954

RESULT 14

DQ034795

LOCUS DQ034795 1008 bp DNA linear GSS 02-JUN-2005

DEFINITION Homo sapiens MAGEA3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION DQ034795

VERSION DQ034795.1 GI:66886004

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1008)

AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees

JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)

PUBMED 15869325

REFERENCE 2 (bases 1 to 1008)

AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES Location/Qualifiers
source 1..1008
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
gene <1..>1008
/gene="MAGEA3"
/locus_tag="HC4231"

ORIGIN

Query Match 12.0%; Score 678.4; DB 14; Length 1008;
Best Local Similarity 81.3%; Pred. No. 6.9e-158;
Matches 820; Conservative 0; Mismatches 166; Indels 22; Gaps 2;

```
Qy      3818 CTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTC 3877
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1   CAGTGGGTCTCCATTGCCCAGCTCCTGCCCACACTCCCGCCTGTTGCCCTGACCAGAGTC 60

Qy      3878 ATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAA 3937
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 ATCATGCCTCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCTTGAGGCCCGA 120

Qy      3938 CAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCT-----GCCACC 3976
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 GGAGAGGCCCTGGGCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGGCTGCC 180

Qy      3977 TCCTCCTCCTCCTCCTCTGGTCCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACA 4036
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 TCCTCCTCTTCTACTCTAGTTGAAGTCACCCCTGGGGGAGGTGCCTGCTGCCGAGTCACCA 240

Qy      4037 GATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGA 4096
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      241 GATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCCACTACCATGAACCTACCTCTC 300

Qy      4097 CAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGT 4156
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      301 TGGAGCCAATCCTATGAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCCCT 360

Qy      4157 ATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTT 4216
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      361 GACCTGGAGTCTGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCGAGTTGGTTTCATTTT 420

Qy      4217 CTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTC 4276
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      421 CTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTGTC 480

Qy      4277 ATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCGAG 4336
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      481 GTCGGAAATTGGCAGTATTTCTTTCTGTGATCTTCAGCAAAGCTTCCAGTTCCCTTGCGAG 540

Qy      4337 CTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCAACGGCCACTCCATGTCCTTGTC 4396
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      541 CTGGTCTTTGGCATCGAGCTGATGGAAGTGGAACCCATCGGCCACTTGTACATCTTTGCC 600

Qy      4397 ACCTGCCTAGGTCTCTCCTATGATGGCTGCTGGGTGATAATCAGATCATGCCCAAGACA 4456
```

```

Db      601  ACCTGCCTGGGCCTCTCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGGCA 660
Qy      4457 GGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAG 4516
      ||| ||||| ||||| ||| || |||| ||||| | ||| ||||| |||
Db      661  GGCTTCCTGATAATCGTCCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 720
Qy      4517 GAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTAT 4576
      ||||| ||||| ||||| ||| ||||| ||| ||||| ||| |||
Db      721  AAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTGAGGGGAGGGAAGACAGTATCTTG 780
Qy      4577 GGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGG 4635
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db      781  GGGGATCCCAAGAAGCTGCTCACCCAACATTTCTGTCAGGAAAAGTACCTGGAGTACCGG 840
Qy      4636 CAGGTGCCCGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT 4695
      ||||| ||| | ||||| ||| | |||| | ||||| ||||| ||||| |||
Db      841  CAGGTCCCGGACAGTGATCCTGCATGTTATGAATTCTGTGGGGTCCAAGGGCCCTCGTT 900
Qy      4696 GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT 4755
      ||||| ||||| ||||| ||| || || || || ||||| || || || ||
Db      901  GAAACCAGCTATGTGAAAGTCCTGCACCATATGGTAAAGATCAGTGGAGGACCTCACATT 960
Qy      4756 TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGA 4803
      | || |||| ||||| ||| | ||||| ||||| ||||| ||
Db      961  TCCTACCCACCCCTGCATGAGTGGGTTTTGAGAGAGGGGGAAGAGTGA 1008

```

RESULT 15

BQ224380

LOCUS BQ224380 811 bp mRNA linear EST 02-MAY-2002

DEFINITION AGENCOURT_7549013 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059308
5', mRNA sequence.

ACCESSION BQ224380

VERSION BQ224380.1 GI:20405780

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 811)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13325 row: m column: 05

High quality sequence stop: 591.

FEATURES

source

Location/Qualifiers

1..811

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

```

/clone="IMAGE:6059308"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies. "

```

ORIGIN

```

Query Match          11.9%;  Score 675.8;  DB 3;  Length 811;
Best Local Similarity 97.4%;  Pred. No. 2.9e-157;
Matches 708;  Conservative 0;  Mismatches 17;  Indels 2;  Gaps 2;

```

```

Qy      3816 GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875
          |||
Db      63  GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGTTGCCCTGACGAGAG 122

Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCC 3935
          |||
Db      123 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCC 182

Qy      3936 AACAAAGAGGCCCTGGGCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCTCTCTCTGG 3995
          |||
Db      183 AACAAAGAGGCCCTGGGCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCTCTCTCTGG 242

Qy      3996 TCCTGGGCACCCTGGAGGAGGTGCCCAGTCTGGGTCAACAGATCCTCCCCAGAGTCCTC 4055
          |||
Db      243 TCCTGGGCACCCTGGAGGAGGTGCCCAGTCTGGGTCAACAGATCCTCCCCAGAGTCCTC 302

Qy      4056 AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGG 4115
          |||
Db      303 AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGG 362

Qy      4116 GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCTTGTTC 4175
          |||
Db      363 GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCTTGTTC 422

Qy      4176 GAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAG 4235
          |||
Db      423 GAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAG 482

Qy      4236 CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACT 4295
          |||
Db      483 CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACT 542

Qy      4296 GTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACG 4355
          |||
Db      543 GTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACG 602

Qy      4356 TGAAGGAAGCAGACCCACCGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCT 4415
          |||
Db      603 TGAAGGAAGCAGACCCACCGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCT 662

Qy      4416 ATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCC 4475
          |||
Db      663 ATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCC 722

Qy      4476 TGGTCAT-GATTGCAATGGAGGGCGGCCATGCTCCT-GAGGAGGAAATCTGGGAGGAGCT 4533
          |||
Db      723 TGGCCATGGATTGCAATGGAGGGCGGCCATGCTCCTGGAGAAGGAAATCTGGAAGAAGT 782

```

Qy 4534 GAGTGTG 4540
|| || |
Db 783 GACTGGG 789

Search completed: August 26, 2006, 01:19:37
Job time : 24236 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e- 26.rag.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-26.rag.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2006, 00:50:36 ; Search time 196 Seconds
(without alignments)
20.995 Million cell updates/sec

Title: US-08-819-669E-26
Perfect score: 52
Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqpl980s:*
2: geneseqpl990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	52	100.0	9	2	AAR29769	Aar29769 Antigen E
2	52	100.0	9	2	AAR63675	Aar63675 Synthetic
3	52	100.0	9	2	AAR50281	Aar50281 MAGE-1 no
4	52	100.0	9	2	AAY38303	Aay38303 MAGE-deri
5	52	100.0	9	2	AAR47330	Aar47330 HLA-A1 MA
6	52	100.0	9	2	AAR49224	Aar49224 HLA-A1 MA
7	52	100.0	9	2	AAR78824	Aar78824 MAGE-1 cy
8	52	100.0	9	2	AAR82988	Aar82988 P815 anti
9	52	100.0	9	2	AAR83932	Aar83932 MHC class
10	52	100.0	9	2	AAR65112	Aar65112 MAGE 1 im
11	52	100.0	9	2	AAR65135	Aar65135 MAGE 1 im
12	52	100.0	9	2	AAR75954	Aar75954 Melanoma
13	52	100.0	9	2	AAR99343	Aar99343 MAGE-1 no
14	52	100.0	9	2	AAR90692	Aar90692 Human leu
15	52	100.0	9	2	AAW00897	Aaw00897 Human mel
16	52	100.0	9	2	AAW54622	Aaw54622 Peptide f
17	52	100.0	9	2	AAW78838	Aaw78838 MAGE-1 pr
18	52	100.0	9	2	AAW77125	Aaw77125 gp75/TRP-
19	52	100.0	9	2	AAW68371	Aaw68371 Human MAG
20	52	100.0	9	2	AAW75734	Aaw75734 Peptidase
21	52	100.0	9	2	AAW75736	Aaw75736 Peptidase
22	52	100.0	9	2	AAY02137	Aay02137 Peptide u
23	52	100.0	9	2	AAW56729	Aaw56729 MAGE-1 an
24	52	100.0	9	2	AAW98945	Aaw98945 HLA-A1 bi
25	52	100.0	9	2	AAY10424	Aay10424 HLA Class
26	52	100.0	9	2	AAY10623	Aay10623 Peptide a
27	52	100.0	9	2	AAY10633	Aay10633 Peptide a
28	52	100.0	9	2	AAY40228	Aay40228 Amino aci
29	52	100.0	9	2	AAY45884	Aay45884 Immunogen
30	52	100.0	9	2	AAY46334	Aay46334 Immunogen
31	52	100.0	9	2	AAY33147	Aay33147 Human MAG
32	52	100.0	9	2	AAY25177	Aay25177 MAGE-1 pe
33	52	100.0	9	2	AAY23250	Aay23250 Peptide d
34	52	100.0	9	2	AAY53541	Aay53541 Human MAG
35	52	100.0	9	2	AAY26884	Aay26884 Tumour-de
36	52	100.0	9	2	AAY22126	Aay22126 Tumour re
37	52	100.0	9	2	AAY00685	Aay00685 Tumour an
38	52	100.0	9	2	AAY49637	Aay49637 Tumour an
39	52	100.0	9	2	AAY01727	Aay01727 Exemplary
40	52	100.0	9	3	AAY71494	Aay71494 Human MAG
41	52	100.0	9	3	AAY90778	Aay90778 Human leu
42	52	100.0	9	3	AAB13741	Aab13741 Peptide f
43	52	100.0	9	3	AAY96509	Aay96509 MAGE-1 no
44	52	100.0	9	3	AAB33650	Aab33650 MHC class
45	52	100.0	9	3	AAB23659	Aab23659 Cytotoxic

ALIGNMENTS

RESULT 1
 AAR29769
 ID AAR29769 standard; peptide; 9 AA.
 XX
 AC AAR29769;
 XX
 DT 25-MAR-2003 (revised)

DT 22-APR-1993 (first entry)
 XX
 DE Antigen E peptide.
 XX
 KW Antigen; tumorigenic cell; A+ B+; T-cell; response; syngeneic; animal;
 KW mouse; tumour rejection antigen precursor; TRAP; PlA.
 XX
 OS Homo sapiens.
 XX
 PN WO9220356-A1.
 XX
 PD 26-NOV-1992.
 XX
 PF 22-MAY-1992; 92WO-US004354.
 XX
 PR 23-MAY-1991; 91US-00705702.
 PR 09-JUL-1991; 91US-00728838.
 PR 23-SEP-1991; 91US-00764364.
 PR 12-DEC-1991; 91US-00807043.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Boon T, Van Der Bruggen P, Van Den Eynde B, Van Pel A, De Plaen E;
 PI Lurquin C, Chomez P, Traversari C;
 XX
 DR WPI; 1992-415460/50.
 XX
 PT Nucleic acid mol. encoding a human tumour rejection antigen precursor -
 PT useful as an immunostimulant in a vaccine for treating and preventing
 PT cancers, also useful in diagnosis.
 XX
 PS Disclosure; Page 97; 142pp; English.
 XX
 CC This sequence represents the sequence of the antigen E. Antigens such as
 CC this one cause a T-cell response to be elicited which transplanted into a
 CC syngeneic animal; usually a mouse. This antigen is derived from the cell
 CC line MEL3.1. See also AAQ32351. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EADPTGHSY 9
 |||||
 Db 1 EADPTGHSY 9

RESULT 2
 AAR63675

ID AAR63675 standard; protein; 9 AA.
 XX
 AC AAR63675;
 XX
 DT 25-MAR-2003 (revised)
 DT 22-JUN-1995 (first entry)
 XX
 DE Synthetic peptide derived from exon 3.1 of MAGE 1.
 XX

KW Melanoma antigen-1; MAGE-1; cytolytic T cells; antigen E; exon 3.1.
 XX
 OS Synthetic.
 XX
 PN WO9423031-A1.
 XX
 PD 13-OCT-1994.
 XX
 PF 17-MAR-1994; 94WO-US002877.
 XX
 PR 26-MAR-1993; 93US-00037230.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Gaugler B, Van Den Eynde B, Boon-Falleur T, Van Der Bruggen P;
 XX
 DR WPI; 1994-333192/41.
 XX
 PT New tumour rejection antigen precursor MAGE3 - useful in treatment and
 PT diagnosis of cancer.
 XX
 PS Example 34; Page 36; 105pp; English.
 XX
 CC AAR63675 is a synthetic peptide derived from exon 3.1 of melanoma antigen
 CC -1 (MAGE-1), it was used to transfer antigen-E cytolytic T lymphocyte
 CC sensitivity to normally non-sensitive cells. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 |||||
 Db 1 EADPTGHSY 9

RESULT 3

AAR50281

ID AAR50281 standard; protein; 9 AA.

XX

AC AAR50281;

XX

DT 25-MAR-2003 (revised)

DT 26-SEP-1994 (first entry)

XX

DE MAGE-1 nonapeptide.

XX

KW MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA;

KW histocompatibility; human leucocyte antigen; probe; treatment; therapy;

KW vaccine.

XX

OS Synthetic.

XX

PN WO9405304-A1.

XX

PD 17-MAR-1994.

XX

PF 30-AUG-1993; 93WO-US008157.

```

XX
PR 31-AUG-1992; 92US-00938334.
PR 26-MAR-1993; 93US-00037230.
PR 07-JUN-1993; 93US-00073103.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, Van Der Bruggen P, De Plaen E, Lurquin C;
PI Traversari C;
XX
DR WPI; 1994-100844/12.
DR N-PSDB; AAQ44751.
XX
PT New nona:peptide derived from tumour rejection antigen precursor -
PT presented by HLA-A1 cancer cells, for use in diagnosis or therapy of esp.
PT melanoma and breast cancer.
XX
PS Disclosure; Page 19; 33pp; English.
XX
CC An isolated nonapeptide having the amino acid sequence Glu-Val-Asp- Pro-
CC Ile-Gly-His-Leu-Tyr is derived from the tumour rejection antigen
CC precursor encoded by the MAGE-3 gene and presented by HLA-A1. The
CC nonapeptide can be used in a vaccine to treat a cancerous condition
CC involving HLA-A1 subtype cancerous cells. The nucleic acid encoding the
CC nonapeptide can be used as a probe to identify tumour cells. This
CC sequence is homologous to the peptide described and is encoded by the
CC MAGE-1 gene. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25
CC -MAR-2003 to correct PI field.)
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
   |||||
Db 1 EADPTGHSY 9

RESULT 4
AAY38303
ID AAY38303 standard; peptide; 9 AA.
XX
AC AAY38303;
XX
DT 29-SEP-1999 (first entry)
XX
DE MAGE-derived HLA-binding peptide.
XX
KW Immunogen; HLA; human leukocyte antigen; binding motif; antiviral; MHC;
KW major histocompatibility complex; viral infection; anticancer;
KW prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9403205-A1.
XX
PD 17-FEB-1994.
XX
PF 06-AUG-1993; 93WO-US007421.

```

XX
 PR 07-AUG-1992; 92US-00926666.
 PR 05-MAR-1993; 93US-00027746.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Kubo RT, Grey HM, Sette A, Celis E;
 XX
 DR WPI; 1994-065403/08.
 XX
 PT Peptide which specifically binds selected MHC allele - used to induce an
 PT immune response for treatment or prevention of viral infection or cancer,
 PT or for diagnosis.
 XX
 PS Disclosure; Page 112; 150pp; English.
 XX
 CC The sequence is a specific example of a group of new immunogenic peptides
 CC having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding motif. For
 CC example, the peptides having an HLA-A3.2 binding motif each have 9-10
 CC residues and contain, from the N-terminus to the C-terminus, (a) a first
 CC conserved residue selected from L, M, I, V, S, A, T, F, C, G, D and E and
 CC (b) a second conserved residue of K, R, Y, H or F, where the first and
 CC second conserved residues are separated by 6-7 residues. The peptides are
 CC capable of binding selected MHC molecules and inducing an immune
 CC response. They can be used to treat and/or prevent viral infection and
 CC cancer, e.g. prostate cancer, lymphoma, hepatitis or AIDS. They can also
 CC be used to produce antibodies for use as diagnostic or therapeutic
 CC agents. The peptides can also be used as diagnostic agents
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 |||||
 Db 1 EADPTGHSY 9

RESULT 5

AAR47330

ID AAR47330 standard; protein; 9 AA.

XX

AC AAR47330;

XX

DT 14-MAY-2003 (revised)

DT 25-MAR-2003 (revised)

DT 31-AUG-1994 (first entry)

XX

DE HLA-A1 MAGE 1 antigen peptide fragment 161-169.

XX

KW Immunogenic; HLA-A3.2; HLA-A1; HLA-A11; binding motif; MHC molecule;

KW immune response; viral infection; cancer; prostate cancer; lymphoma;

KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.

XX

OS Synthetic.

XX

PN WO9403205-A1.

XX

PD 17-FEB-1994.

XX
 PF 06-AUG-1993; 93WO-US007421.
 XX
 PR 07-AUG-1992; 92US-00926666.
 PR 05-MAR-1993; 93US-00027746.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Kubo RT, Grey HM, Sette A, Celis E;
 XX
 DR WPI; 1994-065403/08.
 XX
 PT Peptide which specifically binds selected MHC allele - used to induce an
 PT immune response for treatment or prevention of viral infection or cancer,
 PT or for diagnosis.
 XX
 PS Example 8; Page 52; 150pp; English.
 XX
 CC The sequences given in AAR47304-33 and AAR49201-44 are immunogenic
 CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif. These
 CC peptides may be used in the composition of the invention. These peptides
 CC are capable of binding selected MHC molecules and inducing an immune
 CC response. They can be used to treat and/or prevent viral infection and
 CC cancer, eg. prostate cancer, lymphoma, hepatitis or AIDS. They can also
 CC be used to produce antibodies for use as diagnostic or therapeutic
 CC agents. The peptides can also be used as diagnostic agents. (Updated on
 CC 25-MAR-2003 to correct PN field.) (Updated on 14-MAY-2003 to correct PS
 CC field.)
 XX
 SQ Sequence 9 AA;

 Query Match 100.0%; Score 52; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 EADPTGHSY 9
 |||||
 Db 1 EADPTGHSY 9

 RESULT 6
 AAR49224
 ID AAR49224 standard; protein; 9 AA.
 XX
 AC AAR49224;
 XX
 DT 14-MAY-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 31-AUG-1994 (first entry)
 XX
 DE HLA-A1 MAGE 1 antigen peptide fragment 958.01.
 XX
 KW Immunogenic; HLA-A3.2; HLA-A1; HLA-A11; binding motif; MHC molecule;
 KW immune response; viral infection; cancer; prostate cancer; lymphoma;
 KW hepatitis; AIDS; antibody; diagnosis; melanoma antigen.
 XX
 OS Synthetic.
 XX
 PN W09403205-A1.
 XX
 PD 17-FEB-1994.

```

XX
PF 06-AUG-1993; 93WO-US007421.
XX
PR 07-AUG-1992; 92US-00926666.
PR 05-MAR-1993; 93US-00027746.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Kubo RT, Grey HM, Sette A, Celis E;
XX
DR WPI; 1994-065403/08.
XX
PT Peptide which specifically binds selected MHC allele - used to induce an
PT immune response for treatment or prevention of viral infection or cancer,
PT or for diagnosis.
XX
PS Example 16; Page 116; 150pp; English.
XX
CC The sequences given in AAR47304-33 and AAR49201-44 are immunogenic
CC peptides which have a HLA-A3.2, HLA-A1 or a HLA-A11 binding motif. These
CC peptides may be used in the composition of the invention. These peptides
CC are capable of binding selected MHC molecules and inducing an immune
CC response. They can be used to treat and/or prevent viral infection and
CC cancer, eg. prostate cancer, lymphoma, hepatitis or AIDS. They can also
CC be used to produce antibodies for use as diagnostic or therapeutic
CC agents. The peptides can also be used as diagnostic agents. (Updated on
CC 25-MAR-2003 to correct PN field.) (Updated on 14-MAY-2003 to correct PS
CC field.)
XX
SQ Sequence 9 AA;

Query Match          100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

RESULT 7
AAR78824
ID AAR78824 standard; peptide; 9 AA.
XX
AC AAR78824;
XX
DT 26-MAR-1996 (first entry)
XX
DE MAGE-1 cytotoxic T lymphocyte epitope.
XX
KW MAGE-1; cytotoxic T; CTL; epitope; helper T; HTL; lymphocyte; cell;
KW viruses; parasites; tumours; antigens; disease prevention; treatment.
XX
OS Homo sapiens.
XX
PN WO9522317-A1.
XX
PD 24-AUG-1995.
XX
PF 16-FEB-1995; 95WO-US002121.
XX

```

PR 16-FEB-1994; 94US-00197484.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Vitiello MA, Chesnut RW, Sette AD, Celis E, Grey H;
 XX
 DR WPI; 1995-302545/39.
 XX
 PT Compsn. inducing cytotoxic T lymphocyte response to pref. viral,
 PT bacterial, parasitic or tumour antigens - useful in the treatment and
 PT prevention of diseases associated with the antigen e.g. hepatitis B.
 XX
 PS Disclosure; Page 17; 109pp; English.
 XX
 CC A compsn. which induces a cytotoxic T lymphocyte (CTL) response to an
 CC antigen (Ag) in a mammal comprises, a CTL Ag response inducing peptide
 CC (i.e. AAR78824-R78853) and a lipid conjugated helper T cell inducing
 CC peptide. The compsn. induces a CTL response to bacterial, viral or tumour
 CC Ags, and is therefore useful in the treatment and prevention of diseases
 CC associated with the Ag
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 |||||
 Db 1 EADPTGHSY 9

RESULT 8
 AAR82988
 ID AAR82988 standard; peptide; 9 AA.
 XX
 AC AAR82988;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-FEB-1996 (first entry)
 XX
 DE P815 antigenic peptide.
 XX
 KW P815 antigen; P1A antigen; cancer; vaccine.
 XX
 OS Synthetic.
 XX
 PN WO9523874-A1.
 XX
 PD 08-SEP-1995.
 XX
 PF 23-FEB-1995; 95WO-US002203.
 XX
 PR 01-MAR-1994; 94US-00204727.
 PR 10-MAR-1994; 94US-00209172.
 PR 01-SEP-1994; 94US-00299849.
 PR 30-NOV-1994; 94US-00346774.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI De Plaen E, Boon-Falleur T, Lethe B, Szikora J, De Smet C;

PI Chomez P, Gaugler B, Van Den Eynde B, Brasseur F, Patard J;
 PI Weynants P, Marchand M, Van Der Bruggen P;
 XX
 DR WPI; 1995-320586/41.
 XX
 PT Determn. of cancerous condition(s) - using a nucleic acid as a primer to
 PT determine expression of a MAGE tumour rejection antigen precursor.
 XX
 PS Example 13; Page 22; 121pp; English.
 XX
 CC Using the sequence of the P815A antigen precursor gene P1A (AAT01176), an
 CC antigenic peptide (AAR82988) which was A+B+ (i.e. characteristic of cells
 CC which express both A and B antigens) was produced. The peptide lysed
 CC PO.HTR cells in the presence of cytolytic T lymphocyte cell lines, and
 CC may be useful as a vaccine component. (Updated on 25-MAR-2003 to correct
 CC PI field.)
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 |||||
 Db 1 EADPTGHSY 9

RESULT 9
 AAR83932
 ID AAR83932 standard; peptide; 9 AA.
 XX
 AC AAR83932;
 XX
 DT 05-JUN-1996 (first entry)
 XX
 DE MHC class I restricted antigenic peptide #2.
 XX
 KW MHC class I; antigen; MAGE; melanoma; breast cancer; bladder cancer;
 KW Titermax; cytotoxic T-lymphocyte; tumour; pathogenic disease; bacteria;
 KW parasite; human; animal.
 XX
 OS Synthetic.
 XX
 PN WO9528958-A1.
 XX
 PD 02-NOV-1995.
 XX
 PF 21-APR-1995; 95WO-US004975.
 XX
 PR 22-APR-1994; 94US-00233496.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 PI Nikolic-Zugic J, Dyall R;
 XX
 DR WPI; 1995-382848/49.
 XX
 PT Cytotoxic T-cell induction by MHC class I-restricted peptide in adjuvant
 PT - useful for treating tumours and bacterial or parasitic pathogenic
 PT diseases.

XX
 PS Claim 11; Page 38; 50pp; English.
 XX
 CC The sequences given in AAR83931-49 are MHC class I restricted 8-12 amino
 CC acid antigenic peptides. This peptide is derived from MAGE and is present
 CC in melanoma, breast and bladder cancer. These peptides may be
 CC administered to a subject in combination with a suitable adjuvant, pref.
 CC Titermax (RTM), to induce cytotoxic T- lymphocytes. This method may be
 CC used in the treatment of a tumour or a pathogenic disease, esp. diseases
 CC of bacterial or parasitic origin, in humans and animals, e.g monkeys,
 CC dogs cows, horses, etc
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 |||||
 Db 1 EADPTGHSY 9

RESULT 10

AAR65112

ID AAR65112 standard; peptide; 9 AA.

XX

AC AAR65112;

XX

DT 25-MAR-2003 (revised)

DT 06-OCT-1995 (first entry)

XX

DE MAGE 1 immunogenic peptide 161-169.

XX

KW MAGE 1; immunogenic peptide 161-169; cytotoxic C cells;

KW in vitro activation; cancer; AIDS; bacterial infections; malaria;

KW fungal infections; tuberculosis; hepatitis.

XX

OS Homo sapiens.

XX

PN WO9504817-A1.

XX

PD 16-FEB-1995.

XX

PF 01-AUG-1994; 94WO-US008672.

XX

PR 06-AUG-1993; 93US-00103401.

XX

PA (CYTE-) CYTEL CORP.

XX

PI Celis E, Kubo R, Serra H, Tsai V, Wentworth P;

XX

DR WPI; 1995-090895/12.

XX

PT In vitro activation of cytotoxic T cells for selected killing of target
 PT cells - for treating e.g. cancer, AIDS, hepatitis etc.by incubating them
 PT with antigen presenting cells loaded with appropriate immunogenic
 PT peptide.

XX

PS Example 3; Page 35; 53pp; English.

XX

CC AAR65109-R65145 are immunogenic peptides, they are used in a new method
CC for the in vitro activation of cytotoxic T cells (CTC). This is achieved
CC by incubating the CTCs with antigen presenting cells loaded with an
CC appropriate immunogenic peptide (e.g. one of the above peptides). By
CC selecting the peptides used the following diseases and infections can be
CC treated; cancer, AIDS, hepatitis, other viral and bacterial infections,
CC malaria and tuberculosis. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9

|||||||

Db 1 EADPTGHSY 9

RESULT 11

AAR65135

ID AAR65135 standard; peptide; 9 AA.

XX

AC AAR65135;

XX

DT 25-MAR-2003 (revised)

DT 09-OCT-1995 (first entry)

XX

DE MAGE 1 immunogenic peptide A01.

XX

KW MAGE 1; immunogenic peptide A01; cytotoxic C cells; in vitro activation;

KW cancer; AIDS; bacterial infections; malaria; fungal infections;

KW tuberculosis; hepatitis.

XX

OS Homo sapiens.

XX

PN WO9504817-A1.

XX

PD 16-FEB-1995.

XX

PF 01-AUG-1994; 94WO-US008672.

XX

PR 06-AUG-1993; 93US-00103401.

XX

PA (CYTE-) CYTEL CORP.

XX

PI Celis E, Kubo R, Serra H, Tsai V, Wentworth P;

XX

DR WPI; 1995-090895/12.

XX

PT In vitro activation of cytotoxic T cells for selected killing of target
PT cells - for treating e.g. cancer, AIDS, hepatitis etc.by incubating them
PT with antigen presenting cells loaded with appropriate immunogenic
PT peptide.

XX

PS Example 3; Page 38; 53pp; English.

XX

CC AAR65109-R65145 are immunogenic peptides, they are used in a new method
CC for the in vitro activation of cytotoxic T cells (CTC). This is achieved
CC by incubating the CTCs with antigen presenting cells loaded with an
CC appropriate immunogenic peptide (e.g. one of the above peptides). By

CC selecting the peptides used the following diseases and infections can be
CC treated; cancer, AIDS, hepatitis, other viral and bacterial infections,
CC malaria and tuberculosis. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 12

AAR75954

ID AAR75954 standard; peptide; 9 AA.

XX

AC AAR75954;

XX

DT 06-MAR-1996 (first entry)

XX

DE Melanoma antigen (MAGE-1) epitope.

XX

KW MAGE-3; melanoma antigen; vaccine; immune response; immunogenic peptide;

KW cytotoxic T lymphocyte response; CTL; melanoma; breast cancer; antibody.

XX

OS Homo sapiens.

XX

PN WO9519783-A1.

XX

PD 27-JUL-1995.

XX

PF 25-JAN-1995; 95WO-US001000.

XX

PR 25-JAN-1994; 94US-00186266.

XX

PA (CYTE-) CYTEL CORP.

XX

PI Kubo RT, Grey HM, Sette A, Celis E;

XX

DR WPI; 1995-269270/35.

XX

PT Immunogenic peptide(s) that induce immune response to cancer cells - that

PT express a MAGE-3 protein peptide epitope used in vaccines or adoptive

PT immuno:therapy to induce cytotoxic T lymphocytes.

XX

PS Example; Page 33; 44pp; English.

XX

CC AAR75954 is derived from MAGE-1 protein. It was used to show the

CC specificity of CTL response to MAGE-3 peptides shown in AAR75942-53.

CC AAR75942 is derived from the sequence of the melanoma antigen (MAGE-3)

CC protein and can be used to elicit a primary cytotoxic T lymphocyte

CC response against cells expressing MAGE-3. Synthetic peptides AAR75945-53

CC can be used therapeutically to elicit CTL responses to melanoma, breast,

CC colon, prostate, or other cells which express proteins with this epitope.

CC The peptides have specific HLA-A1 binding capacity

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.1e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 |||||
 Db 1 EADPTGHSY 9

RESULT 13

AAR99343

ID AAR99343 standard; protein; 9 AA.

XX

AC AAR99343;

XX

DT 22-APR-1997 (first entry)

XX

DE MAGE-1 nonapeptide.

XX

KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;

KW tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;

KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;

KW therapy.

XX

OS Homo sapiens.

XX

PN WO9626214-A1.

XX

PD 29-AUG-1996.

XX

PF 01-FEB-1996; 96WO-US001489.

XX

PR 23-FEB-1995; 95US-00393273.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Boon-Falleur T, Van Der Bruggen P, De Plaen E, Lurquin C;

PI Gaugler B, Van Den Eynde B, Traversari C, Romero P;

XX

DR WPI; 1996-402317/40.

DR N-PSDB; AAT35408.

XX

PT New nona:peptide(s) that bind to HLA molecule(s) and induce lysis - by
 PT specific cytolytic T cells, for diagnosis and treatment of tumours and to
 PT expand T cells in vitro.

XX

PS Example 4; Fig 4; 41pp; English.

XX

CC AAR99343-R99350 represent MAGE nonapeptides, based on the tumour
 CC rejection antigen region of the full length MAGE sequences. These
 CC peptides were used to design the nonapeptides of the invention (see
 CC AAR99337-R99342), which bind to a HLA molecule on a cell, and provoke
 CC lysis by cytolytic T cells (CTLs) specific for a complex of the HLA
 CC molecule and nonapeptide. The nonapeptides can be used diagnostically to
 CC identify tumours expressing a particular HLA molecule, or to identify
 CC cancer cells. The peptides can also be used therapeutically, to induce a
 CC CTL response to tumours (where the peptides are optionally coupled to
 CC tumour-specific antibodies), or to induce a response by CTLs that are
 CC otherwise inactive. The peptide sequences may also be used to expand
 CC specific CTLs in vitro for later return to the patient, such as for
 CC treating melanoma. Tumour cells can be identified by using DNA encoding

CC the nonapeptides as probes. Non-human cells transformed with the HLA-A1
CC gene and a DNA sequence encoding one of the peptides, can be used to
CC generate CTLs, or to detect the presence of CTLs in human samples. The
CC non-human transformed cells, when polytransformed, are universal effector
CC cells, and can be used in vaccines, or for treating melanoma or breast
CC cancer

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 14

AAR90692

ID AAR90692 standard; peptide; 9 AA.

XX

AC AAR90692;

XX

DT 31-JUL-1996 (first entry)

XX

DE Human leukocyte antigen (HLA-A1) presented peptide MZ2-E.

XX

KW Human leukocyte antigen; HLA-A1; MAGE-1 derived; blood mononuclear cell;

KW BMC; CD8-beta+ cell; cytolytic T cell; CTL cell; treatment; tumour cell;

KW diagnosis; assay; presented peptide.

XX

OS Synthetic.

XX

PN WO9535500-A1.

XX

PD 28-DEC-1995.

XX

PF 14-JUN-1995; 95WO-US007559.

XX

PR 17-JUN-1994; 94US-00261541.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Coulie P, Van Der Bruggen P, Boon-Falleur T;

XX

DR WPI; 1996-058510/06.

XX

PT Prodn. of specific cytolytic T cell sub-populations - by contacting blood

PT mononuclear cells with specific peptide(s) and a population of CD8-

PT beta(+) cells.

XX

PS Claim 5; Page 19; 25pp; English.

XX

CC The present peptide is the human leukocyte antigen (HLA-A1), MAGE-1

CC derived presented peptide, MZ2-E. By contacting a sample of blood

CC mononuclear cells (BMC) with the peptide (which binds directly to HLA-A1

CC mols. on the surface of the BMC) and CD8-beta+ cells (which stimulate

CC peptide/HLA-A1 complex specific CD8-beta+ cells), a peptide/HLA-A1

CC complex specific cytolytic T (CTL) cell subpopulation can be obtd. . The

CC CTL cells obtd. can be administered to a patient to treat tumour cell

CC related conditions, and can be used in diagnostic methods, e.g. in assays
CC for the peptide/HLA-A1 complex
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 15

AAW00897

ID AAW00897 standard; peptide; 9 AA.

XX

AC AAW00897;

XX

DT 23-MAY-1997 (first entry)

XX

DE Human melanoma MAGE1 tumour associated antigen p161-169.

XX

KW Adeno-associated virus; vector; liposome; transfection; dendritic cell;
KW melanoma; MAGE1; adoptive immunotherapy; tumour associated antigen.

XX

OS Homo sapiens.

XX

PN WO9703703-A1.

XX

PD 06-FEB-1997.

XX

PF 19-JUL-1996; 96WO-US012012.

XX

PR 21-JUL-1995; 95US-0001312P.

PR 01-NOV-1995; 95US-0007184P.

PR 01-DEC-1995; 95US-00566286.

XX

PA (RHON) RHONE POULENC RORER PHARM INC.

XX

PI Philip R, Lebkowski JS;

XX

DR WPI; 1997-145208/13.

XX

PT Adeno-associated virus:liposome complexes for transfecting dendritic
PT cells - for inducing immune response, useful for treating e.g. neoplasia
PT or infections.

XX

PS Example 5; Page 58; 134pp; English.

XX

CC Tumour associated antigens (AAW13660-61, AAW00878-903) can be loaded into
CC dendritic cells and used to induce antitumour immunity. Alternatively,
CC the dendritic cells are transfected with adeno associated virus plasmid
CC DNA (which includes DNA encoding the tumour associated antigen) complexed
CC with cationic liposomes. The antigen loaded or transfected dendritic
CC cells can be used to generate tumour antigen-specific cytotoxic T
CC lymphocytes for use in adoptive immunotherapy in a patient having the
CC corresponding tumour. A suitable antigen comprises amino acids 161-169
CC (AAW00897) of human melanoma MAGE1

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.1e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

Search completed: August 25, 2006, 00:54:22
Job time : 199 secs

SCORE 1.3 BuildDate: 12/06/2005

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

start

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

Result	Score	% Query Match	Length	DB	ID	Description
--------	-------	------------------	--------	----	----	-------------

1	52	100.0	9	1	US-07-938-334C-1	Sequence 1, Appli
2	52	100.0	9	1	US-08-073-103A-12	Sequence 12, Appl
3	52	100.0	9	1	US-08-299-849B-26	Sequence 26, Appl
4	52	100.0	9	1	US-08-186-266-1	Sequence 1, Appli
5	52	100.0	9	1	US-08-443-341-12	Sequence 12, Appl
6	52	100.0	9	1	US-08-787-547-49	Sequence 49, Appl
7	52	100.0	9	1	US-08-498-461-4	Sequence 4, Appli
8	52	100.0	9	1	US-08-902-516-21	Sequence 21, Appl
9	52	100.0	9	1	US-08-142-368A-26	Sequence 26, Appl
10	52	100.0	9	1	US-09-036-582-1	Sequence 1, Appli
11	52	100.0	9	1	US-08-986-234-1	Sequence 1, Appli
12	52	100.0	9	2	US-08-967-727-26	Sequence 26, Appl
13	52	100.0	9	2	US-08-354-679C-12	Sequence 12, Appl
14	52	100.0	9	2	US-08-159-339A-99	Sequence 99, Appl
15	52	100.0	9	2	US-08-795-733B-1	Sequence 1, Appli
16	52	100.0	9	2	US-09-183-931-29	Sequence 29, Appl
17	52	100.0	9	2	US-08-393-273E-12	Sequence 12, Appl
18	52	100.0	9	2	US-08-037-230D-26	Sequence 26, Appl
19	52	100.0	9	2	US-09-183-706-4	Sequence 4, Appli
20	52	100.0	9	2	US-09-162-934-1	Sequence 1, Appli
21	52	100.0	9	2	US-09-061-388-21	Sequence 21, Appl
22	52	100.0	9	2	US-09-166-448-45	Sequence 45, Appl
23	52	100.0	9	2	US-09-567-995-4	Sequence 4, Appli
24	52	100.0	9	2	US-09-099-543C-21	Sequence 21, Appl
25	52	100.0	9	2	US-08-443-580F-12	Sequence 12, Appl
26	52	100.0	9	2	US-09-705-160-29	Sequence 29, Appl
27	52	100.0	9	2	US-09-165-863-1	Sequence 1, Appli
28	52	100.0	9	2	US-08-197-484-1	Sequence 1, Appli
29	52	100.0	9	2	US-09-697-884-45	Sequence 45, Appl
30	52	100.0	9	2	US-09-847-185-21	Sequence 21, Appl
31	52	100.0	9	2	US-08-571-263-12	Sequence 12, Appl
32	52	100.0	9	2	US-09-583-850-26	Sequence 26, Appl
33	52	100.0	9	2	US-09-289-350-1	Sequence 1, Appli
34	52	100.0	9	2	US-09-574-749B-1	Sequence 1, Appli
35	52	100.0	9	2	US-09-579-197-26	Sequence 26, Appl
36	52	100.0	9	2	US-09-341-982-88	Sequence 88, Appl
37	52	100.0	9	2	US-09-404-026-26	Sequence 26, Appl
38	52	100.0	9	2	US-09-312-464-26	Sequence 26, Appl
39	52	100.0	9	2	US-09-318-141-1	Sequence 1, Appli
40	52	100.0	9	2	US-09-114-002-1	Sequence 1, Appli
41	52	100.0	9	2	US-09-000-003A-24	Sequence 24, Appl
42	52	100.0	9	2	US-09-169-717E-7	Sequence 7, Appli
43	52	100.0	9	2	US-09-601-729-131	Sequence 131, App
44	52	100.0	9	2	US-09-812-528-1	Sequence 1, Appli
45	52	100.0	9	2	US-09-806-769-1	Sequence 1, Appli

ALIGNMENTS

```

RESULT 1
US-07-938-334C-1
; Sequence 1, Application US/07938334C
; Patent No. 5405940
; GENERAL INFORMATION:
;   APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
;   APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
;   TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
;   TITLE OF INVENTION: MAGE GENES AND USES THEREOF
;   NUMBER OF SEQUENCES: 22

```

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Felfe & Lynch
;   STREET:    805 Third Avenue
;   CITY:     New York City
;   STATE:    New York
;   COUNTRY:   USA
;   ZIP:      10022
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;   COMPUTER:    IBM PS/2
;   OPERATING SYSTEM:  PC-DOS
;   SOFTWARE:    Wordperfect
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/07/938,334C
;   FILING DATE:    31-AUG-1992
;   CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:    Hanson, No. 5405940man D.
;   REGISTRATION NUMBER:  30,946
;   REFERENCE/DOCKET NUMBER:  LUD 293
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (212) 688-9200
;   TELEFAX:   (212) 838-3884
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:   9 amino acid residues
;   TYPE:     amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE:  protein
;   FEATURE:
;   NAME/KEY:  MAGE-1 derived nonapeptide
US-07-938-334C-1

```

```

Query Match          100.0%;  Score 52;  DB 1;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 5e+05;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 2
US-08-073-103A-12
; Sequence 12, Application US/08073103A
; Patent No. 5462871
;   GENERAL INFORMATION:
;   APPLICANT:  Boon-Falleur, Thierry
;   APPLICANT:  van der Bruggen, Pierre
;   APPLICANT:  De Plaen, Etienne
;   APPLICANT:  Lurquin, Christophe
;   APPLICANT:  Traversari, Catia
;   APPLICANT:  Gaugler, Beatrice
;   APPLICANT:  Van den Eynde, Benoit
;   TITLE OF INVENTION:  ISOLATED NONAPEPTIDES DERIVED FROM
;   TITLE OF INVENTION:  MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
;   NUMBER OF SEQUENCES:  22
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Felfe & Lynch
;   STREET:    805 Third Avenue
;   CITY:     New York City

```

```

; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,103A
; FILING DATE: 7-JUNE-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5462871man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-073-103A-12

```

```

Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 3
US-08-299-849B-26
; Sequence 26, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth , Bernard; Szikora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS

```

```

; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5612201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-299-849B-26

```

```

Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

RESULT 4

US-08-186-266-1

; Sequence 1, Application US/08186266

; Patent No. 5662907

; GENERAL INFORMATION:

; APPLICANT: KUBO, Ralph T.

; APPLICANT: GREY, Howard M.

; APPLICANT: SETTE, Alessandro

; APPLICANT: CELIS, Esteban

; TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC

; TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING

; TITLE OF INVENTION: SYNTHETIC PEPTIDE EPITOPES

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

```

;   ADDRESSEE:  Townsend and Townsend Kourie and Crew
;   STREET:  Steuart Street Tower, One Market Plaza
;   CITY:  San Francisco
;   STATE:  California
;   COUNTRY:  US
;   ZIP:  94105-1493
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/186,266
;   FILING DATE:  25-JAN-1994
;   CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/159,339
;   FILING DATE:  29-NOV-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/103,396
;   FILING DATE:  06-AUG-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/027,746
;   FILING DATE:  05-MAR-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/926,666
;   FILING DATE:  07-AUG-1992
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Bastian, Kevin L.
;   REGISTRATION NUMBER:  34,774
;   REFERENCE/DOCKET NUMBER:  14137-50-4
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (415) 543-9600
;   TELEFAX:  (415) 543-5043
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  9 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-186-266-1

```

```

Query Match          100.0%;  Score 52;  DB 1;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 5e+05;
Matches      9;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 5
US-08-443-341-12
; Sequence 12, Application US/08443341
; Patent No. 5695994
; GENERAL INFORMATION:
; APPLICANT:  Boon-Falleur, Thierry
; APPLICANT:  van der Bruggen, Pierre
; APPLICANT:  De Plaen, Etienne
; APPLICANT:  Lurquin, Christophe
; APPLICANT:  Traversari, Catia

```

```

; APPLICANT: Gaugler, Beatrice
; APPLICANT: Van den Eynde, Benoit
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,341
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,103
; FILING DATE: 7-JUNE-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5695994man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-443-341-12

```

```

Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 6
US-08-787-547-49
; Sequence 49, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne

```

```

; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-49

```

```

Query Match          100.0%;  Score 52;  DB 1;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 5e+05;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 7
US-08-498-461-4
; Sequence 4, Application US/08498461
; Patent No. 5827073
; GENERAL INFORMATION:
; APPLICANT: Luescher, Immanuel; Anjuere, Fabienne;
; APPLICANT: Layer, Andreas; Romero, Pedro; Cerottini, Jean-Charles
; TITLE OF INVENTION: Photoreactive Peptide Derivatives
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue

```

```

; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/498,461
; FILING DATE: 5-JULY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5827073man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5403
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-498-461-4

```

```

Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

RESULT 8

US-08-902-516-21

```

; Sequence 21, Application US/08902516
; Patent No. 5891432
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; TITLE OF INVENTION: RESPONSE USING SAME
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,516
; FILING DATE: 29-JUL-1997
; CLASSIFICATION: 424

```

```

; ATTORNEY/AGENT INFORMATION:
;   NAME:  Campbell, Cathryn A.
;   REGISTRATION NUMBER:  31,815
;   REFERENCE/DOCKET NUMBER:  P-IM 2442
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (619)535-9001
;   TELEFAX:  (619)535-8949
; INFORMATION FOR SEQ ID NO:  21:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  9 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-902-516-21

```

```

Query Match          100.0%;  Score 52;  DB 1;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 5e+05;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 9
US-08-142-368A-26
; Sequence 26, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
;   APPLICANT:  Boon-Falleur, Thierry; Van der Bruggen, Thierry;
;   APPLICANT:  Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
;   APPLICANT:  Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
;   TITLE OF INVENTION:  Tumor Rejection Antigen Precursors, Tumor
;   TITLE OF INVENTION:  Rejection Antigens and Uses Thereof
;   NUMBER OF SEQUENCES:  26
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Felfe & Lynch
;     STREET:  805 Third Avenue
;     CITY:  New York City
;     STATE:  New York
;     ZIP:  10022
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette, 5.25 inch, 360 kb storage
;     COMPUTER:  IBM
;     OPERATING SYSTEM:  PC-DOS
;     SOFTWARE:  Wordperfect
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/142,368A
;     FILING DATE:  02-MAY-1994
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US92/04354
;     FILING DATE:  22-MAY-1992
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  07/807,043
;     FILING DATE:  12-DECEMBER-1991
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  07/764,364
;     FILING DATE:  23-SEPTEMBER-1991
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  07/728,838

```

```

; APPLICATION NUMBER: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5925729man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5253.4-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-142-368A-26

```

```

Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 10
US-09-036-582-1
; Sequence 1, Application US/09036582A
; Patent No. 5965381
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Cornelis, Guy R.
; TITLE OF INVENTION: DELIVERY OF PROTEINS INTO EUKARYOTIC CELLS
; TITLE OF INVENTION: WITH RECOMBINANT YERSINIA
; FILE REFERENCE: 11154
; CURRENT APPLICATION NUMBER: US/09/036,582A
; CURRENT FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human MAGE-1 peptide
US-09-036-582-1

```

```

Query Match          100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 11
US-08-986-234-1
; Sequence 1, Application US/08986234
; Patent No. 5981706

```

; GENERAL INFORMATION:
; APPLICANT: Wallen, et al.
; TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
; FILE REFERENCE: UNME-0008-1
; CURRENT APPLICATION NUMBER: US/08/986,234
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: human
US-08-986-234-1

Query Match 100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 12
US-08-967-727-26

; Sequence 26, Application US/08967727
; Patent No. 6025474
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,727
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838

```

; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-967-727-26

```

```

Query Match          100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

RESULT 13

US-08-354-679C-12

```

; Sequence 12, Application US/08354679C
; Patent No. 6034214
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
; APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,679C
; FILING DATE: 13-DECEMBER-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUGUST-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BAER, MADELINE F.
; REGISTRATION NUMBER: 36,437
; REFERENCE/DOCKET NUMBER: LUD 5293.2

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-354-679C-12

```

```

Query Match          100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

RESULT 14

US-08-159-339A-99

```

; Sequence 99, Application US/08159339A
; Patent No. 6037135

```

; GENERAL INFORMATION:

```

; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

```

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

```

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424

```

; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993

```

; ATTORNEY/AGENT INFORMATION:

```

; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US

```

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 99:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-159-339A-99

Query Match 100.0%; Score 52; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 |||||
 Db 1 EADPTGHSY 9

RESULT 15

US-08-795-733B-1

; Sequence 1, Application US/08795733B
 ; Patent No. 6087441

; GENERAL INFORMATION:

; APPLICANT: Ayyoub, Maha; Monsarrat, Bernard; Mazarg
 ; APPLICANT: Honor ; Van Der Eynde, Beno t; Gairin, Jean
 ; APPLICANT: Edouard
 ; TITLE OF INVENTION: Structurally Modified Peptides
 ; TITLE OF INVENTION: Resistant to Peptidase Degradation
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski L.L.P.
 ; STREET: 666 Fifth Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/795,733B
 ; FILING DATE: February 13, 1997
 ; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6087441man D. Hanson
 ; REGISTRATION NUMBER: 30,946
 ; REFERENCE/DOCKET NUMBER: LUD 5461 - JEL/NDH

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-795-733B-1

Query Match 100.0%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9

|||||

Db 1 EADPTGHSY 9

Search completed: August 25, 2006, 01:01:08
Job time : 53 secs

SCORE 1.3 BuildDate: 12/06/2005

1	52	100.0	9	2	US-08-344-824-18	Sequence 18, Appl
2	52	100.0	9	3	US-09-812-528-1	Sequence 1, Appli
3	52	100.0	9	3	US-09-847-185-21	Sequence 21, Appl
4	52	100.0	9	3	US-09-077-214-9	Sequence 9, Appli
5	52	100.0	9	3	US-09-923-831-4	Sequence 4, Appli
6	52	100.0	9	3	US-09-888-721-23	Sequence 23, Appl
7	52	100.0	9	3	US-09-766-889A-8	Sequence 8, Appli
8	52	100.0	9	3	US-09-909-460-49	Sequence 49, Appl
9	52	100.0	9	3	US-09-789-649-21	Sequence 21, Appl
10	52	100.0	9	3	US-09-872-836-49	Sequence 49, Appl
11	52	100.0	9	4	US-10-161-097-1	Sequence 1, Appli
12	52	100.0	9	4	US-10-128-711-1	Sequence 1, Appli
13	52	100.0	9	4	US-10-224-286-21	Sequence 21, Appl
14	52	100.0	9	4	US-10-170-832-45	Sequence 45, Appl
15	52	100.0	9	4	US-10-239-313A-2	Sequence 2, Appli
16	52	100.0	9	4	US-10-164-121A-19	Sequence 19, Appl
17	52	100.0	9	4	US-10-164-078A-18	Sequence 18, Appl
18	52	100.0	9	4	US-10-406-317-15	Sequence 15, Appl
19	52	100.0	9	4	US-10-447-161-9	Sequence 9, Appli
20	52	100.0	9	4	US-10-218-095-11	Sequence 11, Appl
21	52	100.0	9	4	US-10-367-580-139	Sequence 139, App
22	52	100.0	9	4	US-10-367-593-139	Sequence 139, App
23	52	100.0	9	4	US-10-367-594-139	Sequence 139, App
24	52	100.0	9	4	US-10-367-654-139	Sequence 139, App
25	52	100.0	9	4	US-10-367-658-139	Sequence 139, App
26	52	100.0	9	4	US-10-367-668-139	Sequence 139, App
27	52	100.0	9	4	US-10-297-168-15	Sequence 15, Appl
28	52	100.0	9	4	US-10-258-144-35	Sequence 35, Appl
29	52	100.0	9	4	US-10-367-674-139	Sequence 139, App
30	52	100.0	9	4	US-10-415-841A-43	Sequence 43, Appl
31	52	100.0	9	4	US-10-777-053-409	Sequence 409, App
32	52	100.0	9	4	US-10-777-053-616	Sequence 616, App
33	52	100.0	9	4	US-10-777-053-626	Sequence 626, App
34	52	100.0	9	4	US-10-777-053-933	Sequence 933, App
35	52	100.0	9	4	US-10-777-053-934	Sequence 934, App
36	52	100.0	9	4	US-10-725-952-1	Sequence 1, Appli
37	52	100.0	9	4	US-10-758-673-21	Sequence 21, Appl
38	52	100.0	9	4	US-10-753-158-1	Sequence 1, Appli
39	52	100.0	9	4	US-10-837-217-409	Sequence 409, App
40	52	100.0	9	4	US-10-837-217-616	Sequence 616, App
41	52	100.0	9	4	US-10-837-217-626	Sequence 626, App
42	52	100.0	9	4	US-10-837-217-933	Sequence 933, App
43	52	100.0	9	4	US-10-837-217-934	Sequence 934, App
44	52	100.0	9	4	US-10-670-472A-10	Sequence 10, Appl
45	52	100.0	9	5	US-10-362-715-13	Sequence 13, Appl

ALIGNMENTS

```

RESULT 1
US-08-344-824-18
; Sequence 18, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
;   APPLICANT:  SETTE, Alessandro
;   APPLICANT:  SIDNEY, John
;   TITLE OF INVENTION:  HLA BINDING PEPTIDES AND THEIR USES
;   NUMBER OF SEQUENCES:  399
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Townsend and Townsend Khourie and Crew

```

```

; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-18

```

```

Query Match          100.0%;  Score 52;  DB 2;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 1.9e+06;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 2
US-09-812-528-1
; Sequence 1, Application US/09812528
; Patent No. US20010018210A1
; GENERAL INFORMATION:
; APPLICANT: Bachovchin, William
; APPLICANT: Wallner, Barbara
; TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN
; TITLE OF INVENTION: VITRO
; FILE REFERENCE: I0248/7015
; CURRENT APPLICATION NUMBER: US/09/812,528
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/060,306
; PRIOR FILING DATE: 1997-09-29
; PRIOR APPLICATION NUMBER: US 09/162,934
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 3.0

```

; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-812-528-1

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 3

US-09-847-185-21

; Sequence 21, Application US/09847185

; Patent No. US20020076392A1

; GENERAL INFORMATION:

; APPLICANT: Soo Hoo, William

; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS

; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CAMPBELL & FLORES, LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/847,185

; FILING DATE: 01-May-2001

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/201,931

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IM 2442

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)535-9001

; TELEFAX: (619)535-8949

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-847-185-21

Query Match 100.0%; Score 52; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 4

US-09-077-214-9

; Sequence 9, Application US/09077214

; Publication No. US20020085997A1

; GENERAL INFORMATION:

; APPLICANT: Schmidt, Walter

; APPLICANT: Birnstiel, Max

; APPLICANT: Schweighoffer, Tamas

; APPLICANT: Steinlein, Peter

; APPLICANT: Buschle, Michael

; TITLE OF INVENTION: Tumor Vaccine And Process For the

; TITLE OF INVENTION: Preparation Thereof

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 1100 New York Avenue N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/077,214

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE 195 43 649.0

; FILING DATE: 23-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE 196 07 044.9

; FILING DATE: 24-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Fleshner, Raz E.

; REGISTRATION NUMBER: 34,331

; REFERENCE/DOCKET NUMBER: 0652.1710000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-371-2600

; TELEFAX: 202-371-2540

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

US-09-077-214-9

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||||
Db 1 EADPTGHSY 9

RESULT 5

US-09-923-831-4

; Sequence 4, Application US/09923831
; Patent No. US20020115142A1
; GENERAL INFORMATION:
; APPLICANT: Martelange, Val,rie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461/7054
; CURRENT APPLICATION NUMBER: US/09/923,831
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 09/183,706
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-831-4

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||||
Db 1 EADPTGHSY 9

RESULT 6

US-09-888-721-23

; Sequence 23, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-888-721-23

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||||
Db 1 EADPTGHSY 9

RESULT 7

US-09-766-889A-8

; Sequence 8, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-8

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||||
Db 1 EADPTGHSY 9

RESULT 8

US-09-909-460-49

; Sequence 49, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; TITLE OF INVENTION: ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346

;
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-460-49

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 9

US-09-789-649-21
; Sequence 21, Application US/09789649
; Publication No. US20030082804A1
; GENERAL INFORMATION:
; APPLICANT: Valmori, Danila
; APPLICANT: Cerottini, Jean-Charles
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Isolated No. US20030082804A1 - And Decapeptides Which Bind
; TITLE OF INVENTION: To HLA Molecules, and the Use Thereof
; FILE REFERENCE: LUD 5483.2
; CURRENT APPLICATION NUMBER: US/09/789,649
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US09/099,543
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: US 09/061,388
; PRIOR FILING DATE: 1998-04-16
; PRIOR APPLICATION NUMBER: US 08/880,963
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide from MAGE-1 Protein
US-09-789-649-21

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 10

US-09-872-836-49
; Sequence 49, Application US/09872836
; Publication No. US20040142475A1
; GENERAL INFORMATION:
; APPLICANT: Barman, Shikha P.

```

; APPLICANT: McKeever, Una
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 08191-018001
; CURRENT APPLICATION NUMBER: US/09/872,836
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,830
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-836-49

```

```

Query Match          100.0%;  Score 52;  DB 3;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 1.9e+06;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 11
US-10-161-097-1
; Sequence 1, Application US/10161097
; Publication No. US20030096404A1
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/10/161,097
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US/09/574,749
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-10-161-097-1

```

```

Query Match          100.0%;  Score 52;  DB 4;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 1.9e+06;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 12

US-10-128-711-1

; Sequence 1, Application US/10128711

; Publication No. US20030099634A1

; GENERAL INFORMATION:

; APPLICANT: VITIELLO, Maria A.

; CHESTNUT, Robert W.

; SETTE, Alessandro D.

; CELIS, Esteban

; GRAY, Howard

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Kourie and Crew

; STREET: Steuart Street Tower, One Market Plaza

; CITY: San Francisco

; STATE: California

; COUNTRY: US

; ZIP: 94105-1493

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/128,711

; FILING DATE: 22-Apr-2002

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/197,484

; FILING DATE: 16-FEB-1994

; APPLICATION NUMBER: US 07/935,811

; FILING DATE: 26-AUG-1992

; APPLICATION NUMBER: US 07/874,491

; FILING DATE: 27-APR-1992

; APPLICATION NUMBER: US 07/827,682

; FILING DATE: 29-JAN-1992

; APPLICATION NUMBER: US 07/749,568

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Parmelee, Steven W.

; REGISTRATION NUMBER: 31,990

; REFERENCE/DOCKET NUMBER: 14137-26-4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 467-9600

; TELEFAX: (206) 623-6793

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-128-711-1

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||||
Db 1 EADPTGHSY 9

RESULT 13

US-10-224-286-21

; Sequence 21, Application US/10224286

; Publication No. US20030108517A1

; GENERAL INFORMATION:

; APPLICANT: Soo Hoo, William

; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS

; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CAMPBELL & FLORES, LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: United States

; ZIP: 92121

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/224,286

; FILING DATE: 19-Aug-2002

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/902,516

; FILING DATE: 29-JUL-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-IM 2442

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619)535-9001

; TELEFAX: (619)535-8949

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-10-224-286-21

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9

|||||||
Db 1 EADPTGHSY 9

RESULT 14

US-10-170-832-45
; Sequence 45, Application US/10170832
; Publication No. US20030170792A1
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/10/170,832
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-832-45

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||||
Db 1 EADPTGHSY 9

RESULT 15

US-10-239-313A-2
; Sequence 2, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-2

Query Match 100.0%; Score 52; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||||
Db 1 EADPTGHSY 9

Search completed: August 25, 2006, 01:15:15
Job time : 186 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e-26.rapbn.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
---------------------------------	---	---------------------------------------	---------------------------	--

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-26.rapbn.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2006, 01:12:19 ; Search time 32 Seconds
(without alignments)
19.244 Million cell updates/sec

Title: US-08-819-669E-26
Perfect score: 52
Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 247503 seqs, 68422524 residues

Total number of hits satisfying chosen parameters: 247503

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	52	100.0	9	6	US-10-497-088-4	Sequence 4, Appli
2	52	100.0	9	7	US-11-253-240-26	Sequence 26, Appl
3	52	100.0	9	7	US-11-313-152-354	Sequence 354, App
4	52	100.0	9	7	US-11-313-152-553	Sequence 553, App
5	52	100.0	9	7	US-11-313-152-563	Sequence 563, App
6	52	100.0	309	7	US-11-323-049-5	Sequence 5, Appli
7	52	100.0	309	7	US-11-323-964-5	Sequence 5, Appli
8	52	100.0	1052	6	US-10-497-088-21	Sequence 21, Appl
9	52	100.0	1342	6	US-10-497-088-14	Sequence 14, Appl
10	42	80.8	9	7	US-11-313-152-558	Sequence 558, App
11	40	76.9	9	7	US-11-313-152-559	Sequence 559, App
12	37	71.2	1049	6	US-10-539-228-343	Sequence 343, App
13	36	69.2	9	6	US-10-538-066-230	Sequence 230, App
14	36	69.2	9	6	US-10-538-066-231	Sequence 231, App
15	36	69.2	9	6	US-10-506-334-2	Sequence 2, Appli
16	36	69.2	9	6	US-10-506-334-19	Sequence 19, Appl
17	36	69.2	9	7	US-11-313-152-357	Sequence 357, App
18	36	69.2	9	7	US-11-313-152-534	Sequence 534, App
19	36	69.2	9	7	US-11-313-152-535	Sequence 535, App
20	36	69.2	9	7	US-11-313-152-551	Sequence 551, App
21	36	69.2	10	6	US-10-538-066-732	Sequence 732, App
22	36	69.2	11	6	US-10-538-066-229	Sequence 229, App
23	36	69.2	11	6	US-10-538-066-723	Sequence 723, App
24	36	69.2	314	6	US-10-538-066-366	Sequence 366, App
25	36	69.2	314	7	US-11-323-049-6	Sequence 6, Appli
26	36	69.2	314	7	US-11-323-964-6	Sequence 6, Appli
27	36	69.2	518	6	US-10-449-902-48443	Sequence 48443, A
28	35	67.3	293	6	US-10-449-902-53971	Sequence 53971, A
29	35	67.3	302	7	US-11-056-355B-83479	Sequence 83479, A
30	35	67.3	526	7	US-11-056-355B-83478	Sequence 83478, A
31	35	67.3	574	7	US-11-056-355B-83477	Sequence 83477, A
32	35	67.3	1139	6	US-10-449-902-52733	Sequence 52733, A
33	35	67.3	1469	7	US-11-330-403-6435	Sequence 6435, Ap
34	34	65.4	299	7	US-11-293-697-3999	Sequence 3999, Ap
35	34	65.4	393	7	US-11-330-403-827	Sequence 827, App
36	33	63.5	9	7	US-11-313-152-557	Sequence 557, App
37	33	63.5	61	6	US-10-449-902-34383	Sequence 34383, A
38	33	63.5	138	6	US-10-953-349-6081	Sequence 6081, Ap
39	33	63.5	138	7	US-11-056-355B-28382	Sequence 28382, A
40	33	63.5	138	7	US-11-056-355B-30643	Sequence 30643, A
41	33	63.5	138	7	US-11-056-355B-31972	Sequence 31972, A
42	33	63.5	138	7	US-11-056-355B-34233	Sequence 34233, A
43	33	63.5	138	7	US-11-056-355B-97528	Sequence 97528, A
44	33	63.5	138	7	US-11-056-355B-102911	Sequence 102911,
45	33	63.5	138	7	US-11-056-355B-108767	Sequence 108767,

ALIGNMENTS

RESULT 1

US-10-497-088-4

; Sequence 4, Application US/10497088

; Publication No. US20060088520A1

; GENERAL INFORMATION:

; APPLICANT: Crucell Holland B.V.

; APPLICANT: Germeraad, Wilfred

; APPLICANT: Logtenberg, Ton

; APPLICANT: Lekkerkerker, Annemarie N

```

; TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen
; TITLE OF INVENTION: presenting cell contacted with such conjugate, their use for
; TITLE OF INVENTION: vaccination or as medicament, and methods for their production
; TITLE OF INVENTION: generation
; FILE REFERENCE: 0070 US 00 CON
; CURRENT APPLICATION NUMBER: US/10/497,088
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/EP01/14255
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: PCT/EP02/13681
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: EP01204997.9
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE-1.A1 specific peptide
US-10-497-088-4

```

```

Query Match          100.0%; Score 52; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 2
US-11-253-240-26
; Sequence 26, Application US/11253240
; Publication No. US20060127356A1
; GENERAL INFORMATION:
; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;
; van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/253,240
; FILING DATE: 17-Oct-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/579,543
; FILING DATE: 26-May-2000
; APPLICATION NUMBER: 09/583,850

```

```

; FILING DATE:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-11-253-240-26

```

```

Query Match          100.0%;  Score 52;  DB 7;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 2.3e+05;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 3
US-11-313-152-354
; Sequence 354, Application US/11313152
; Publication No. US20060153858A1
; GENERAL INFORMATION:
; APPLICANT: Kundig, Thomas M.
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE
; FILE REFERENCE: MANNK.001CP2C1
; CURRENT APPLICATION NUMBER: US/11/313,152
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/776,232
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/380,534
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US98/14289
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 08/988,320
; PRIOR FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: CA 2,209,815
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 569
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 354
; LENGTH: 9

```

; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-313-152-354

Query Match 100.0%; Score 52; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 4

US-11-313-152-553
; Sequence 553, Application US/11313152
; Publication No. US20060153858A1
; GENERAL INFORMATION:
; APPLICANT: Kundig, Thomas M.
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE
; FILE REFERENCE: MANNK.001CP2C1
; CURRENT APPLICATION NUMBER: US/11/313,152
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/776,232
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/380,534
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US98/14289
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 08/988,320
; PRIOR FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: CA 2,209,815
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 569
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 553
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-313-152-553

Query Match 100.0%; Score 52; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 5

US-11-313-152-563
; Sequence 563, Application US/11313152
; Publication No. US20060153858A1
; GENERAL INFORMATION:
; APPLICANT: Kundig, Thomas M.
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE
; FILE REFERENCE: MANNK.001CP2C1
; CURRENT APPLICATION NUMBER: US/11/313,152

; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/776,232
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/380,534
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US98/14289
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 08/988,320
; PRIOR FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: CA 2,209,815
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 569
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 563
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-313-152-563

Query Match 100.0%; Score 52; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||
Db 1 EADPTGHSY 9

RESULT 6

US-11-323-049-5
; Sequence 5, Application US/11323049
; Publication No. US20060159694A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; APPLICANT: Diamond, David C.
; APPLICANT: Bot, Adrian Ion
; APPLICANT: Liu, Xiping
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.049A
; CURRENT APPLICATION NUMBER: US/11/323,049
; CURRENT FILING DATE: 2005-12-29
; PRIOR APPLICATION NUMBER: 60/640,598
; PRIOR FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-323-049-5

Query Match 100.0%; Score 52; DB 7; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||
Db 161 EADPTGHSY 169

RESULT 7

US-11-323-964-5

```
; Sequence 5, Application US/11323964
; Publication No. US20060159689A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; APPLICANT: Simard, John J.L.
; APPLICANT: Diamond, David C.
; APPLICANT: Bot, Adrian Ion
; APPLICANT: Liu, Xiping
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.050CP1
; CURRENT APPLICATION NUMBER: US/11/323,964
; CURRENT FILING DATE: 2005-12-29
; PRIOR APPLICATION NUMBER: 11/155,288
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: PCT/US2005/021836
; PRIOR FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: 60/580,969
; PRIOR FILING DATE: 2004-06-17
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-323-964-5
```

```
Query Match          100.0%; Score 52; DB 7; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 EADPTGHSY 9
        |||||
Db      161 EADPTGHSY 169
```

RESULT 8

US-10-497-088-21

```
; Sequence 21, Application US/10497088
; Publication No. US20060088520A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Germeraad, Wilfred
; APPLICANT: Logtenberg, Ton
; APPLICANT: Lekkerkerker, Annemarie N
; TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen
; TITLE OF INVENTION: presenting cell contacted with such conjugate, their use for
; TITLE OF INVENTION: vaccination or as medicament, and methods for their production
; TITLE OF INVENTION: generation
; FILE REFERENCE: 0070 US 00 CON
; CURRENT APPLICATION NUMBER: US/10/497,088
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/EP01/14255
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: PCT/EP02/13681
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: EP01204997.9
; PRIOR FILING DATE: 2001-12-19
```

```
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 1052
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: MatDC16-Cgamma4-MAGE-1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (546)..(546)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-497-088-21
```

```
Query Match          100.0%; Score 52; DB 6; Length 1052;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 EADPTGHSY 9
        |||||
Db      904 EADPTGHSY 912
```

RESULT 9

US-10-497-088-14

```
; Sequence 14, Application US/10497088
; Publication No. US20060088520A1
; GENERAL INFORMATION:
; APPLICANT: Crucell Holland B.V.
; APPLICANT: Germeraad, Wilfred
; APPLICANT: Logtenberg, Ton
; APPLICANT: Lekkerkerker, Annemarie N
; TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen
; TITLE OF INVENTION: presenting cell contacted with such conjugate, their use for
; TITLE OF INVENTION: vaccination or as medicament, and methods for their production
; TITLE OF INVENTION: generation
; FILE REFERENCE: 0070 US 00 CON
; CURRENT APPLICATION NUMBER: US/10/497,088
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: PCT/EP01/14255
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: PCT/EP02/13681
; PRIOR FILING DATE: 2002-11-29
; PRIOR APPLICATION NUMBER: EP01204997.9
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 1342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MatDC16-Cgamma4-MAGE-A1
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (836)..(836)
; OTHER INFORMATION: Xaa can be any amino acid
US-10-497-088-14
```

```
Query Match          100.0%; Score 52; DB 6; Length 1342;
Best Local Similarity 100.0%; Pred. No. 0.14;
```

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||||
Db 161 EADPTGHSY 169

RESULT 10

US-11-313-152-558
; Sequence 558, Application US/11313152
; Publication No. US20060153858A1
; GENERAL INFORMATION:
; APPLICANT: Kundig, Thomas M.
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE
; FILE REFERENCE: MANNK.001CP2C1
; CURRENT APPLICATION NUMBER: US/11/313,152
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/776,232
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/380,534
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US98/14289
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 08/988,320
; PRIOR FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: CA 2,209,815
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 569
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 558
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(9)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-11-313-152-558

Query Match 80.8%; Score 42; DB 7; Length 9;
Best Local Similarity 77.8%; Pred. No. 2.3e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||| |||
Db 1 EADPIGHXY 9

RESULT 11

US-11-313-152-559
; Sequence 559, Application US/11313152
; Publication No. US20060153858A1
; GENERAL INFORMATION:
; APPLICANT: Kundig, Thomas M.
; APPLICANT: Simard, John J. L.
; TITLE OF INVENTION: METHOD OF INDUCING A CTL RESPONSE
; FILE REFERENCE: MANNK.001CP2C1
; CURRENT APPLICATION NUMBER: US/11/313,152
; CURRENT FILING DATE: 2005-12-19
; PRIOR APPLICATION NUMBER: 09/776,232

```

; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/380,534
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US98/14289
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 08/988,320
; PRIOR FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: CA 2,209,815
; PRIOR FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 569
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 559
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-11-313-152-559

```

```

Query Match          76.9%;   Score 40;   DB 7;   Length 9;
Best Local Similarity 77.8%;   Pred. No. 2.3e+05;
Matches      7;   Conservative    0;   Mismatches    2;   Indels      0;   Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||| || |
Db      1 EADPIGHLY 9

```

```

RESULT 12
US-10-539-228-343
; Sequence 343, Application US/10539228
; Publication No. US20060154250A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: CHIR0052-101 (PP023370.0003)
; CURRENT APPLICATION NUMBER: US/10/539,228
; CURRENT FILING DATE: 2005-06-17
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-18
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 343
;   LENGTH: 1049
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-539-228-343

```

```

Query Match          71.2%;   Score 37;   DB 6;   Length 1049;
Best Local Similarity 100.0%;   Pred. No. 68;
Matches      6;   Conservative    0;   Mismatches    0;   Indels      0;   Gaps      0;

```

```

Qy      4 PTGHSY 9
        |||||
Db      52 PTGHSY 57

```

```

RESULT 13
US-10-538-066-230
; Sequence 230, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:

```

; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Compositions
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 230
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-230

Query Match 69.2%; Score 36; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.3e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | |
Db 1 EVDPIGHLY 9

RESULT 14

US-10-538-066-231

; Sequence 231, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Compositions
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 231
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-231

Query Match 69.2%; Score 36; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.3e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | |
Db 1 ETDPIGHLY 9

RESULT 15

US-10-506-334-2

; Sequence 2, Application US/10506334
; Publication No. US20060122119A1
; GENERAL INFORMATION:
; APPLICANT: LINARD, BORIS

```

; APPLICANT: JOTEREAU, FRANCINE
; APPLICANT: BENLALAM, HOUSSEM
; APPLICANT: DIEZ, ELIZABETH
; APPLICANT: GUILLOUX, YANNICK
; APPLICANT: LABARRIERE, NATHALIE
; APPLICANT: GERVOIS, NADINE
; APPLICANT: DERRE, LAURENT
; TITLE OF INVENTION: PEPTIDES FOR USE IN ANTITUMOR IMMUNOTHERAPY
; FILE REFERENCE: 258087USOXPCT
; CURRENT APPLICATION NUMBER: US/10/506,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: PCT/FR03/00698
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: FR 02/02703
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-506-334-2

```

```

Query Match          69.2%; Score 36; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.3e+05;
Matches      6; Conservative      0; Mismatches      3; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        | | | | |
Db      1 EVDPIGHVY 9

```

Search completed: August 25, 2006, 01:15:52
Job time : 33 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e 26.rapm.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-81 26.rapm.

[start](#)

[Go Back to previ](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2006, 01:00:27 ; Search time 604 Seconds
(without alignments)
22.753 Million cell updates/sec

Title: US-08-819-669E-26
Perfect score: 52
Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/paa/PCTUS_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/paa/US066_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/paa/US073_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/paa/US074_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/paa/US075_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/paa/US076_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/paa/US077_COMB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/paa/US078_COMB.pep:*
9: /EMC_Celerra_SIDS3/ptodata/2/paa/US079_COMB.pep:*
10: /EMC_Celerra_SIDS3/ptodata/2/paa/US080_COMB.pep:*
11: /EMC_Celerra_SIDS3/ptodata/2/paa/US081_COMB.pep:*
12: /EMC_Celerra_SIDS3/ptodata/2/paa/US082_COMB.pep:*
13: /EMC_Celerra_SIDS3/ptodata/2/paa/US083_COMB.pep:*
14: /EMC_Celerra_SIDS3/ptodata/2/paa/US084_COMB.pep:*
15: /EMC_Celerra_SIDS3/ptodata/2/paa/US085_COMB.pep:*
16: /EMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*
17: /EMC_Celerra_SIDS3/ptodata/2/paa/US087_COMB.pep:*

```

18: /EMC_Celerra_SIDS3/ptodata/2/paa/US088_COMB.pep:*
19: /EMC_Celerra_SIDS3/ptodata/2/paa/US089_COMB.pep:*
20: /EMC_Celerra_SIDS3/ptodata/2/paa/US090_COMB.pep:*
21: /EMC_Celerra_SIDS3/ptodata/2/paa/US091_COMB.pep:*
22: /EMC_Celerra_SIDS3/ptodata/2/paa/US092_COMB.pep:*
23: /EMC_Celerra_SIDS3/ptodata/2/paa/US093_COMB.pep:*
24: /EMC_Celerra_SIDS3/ptodata/2/paa/US094_COMB.pep:*
25: /EMC_Celerra_SIDS3/ptodata/2/paa/US095_COMB.pep:*
26: /EMC_Celerra_SIDS3/ptodata/2/paa/US096_COMB.pep:*
27: /EMC_Celerra_SIDS3/ptodata/2/paa/US097_COMB.pep:*
28: /EMC_Celerra_SIDS3/ptodata/2/paa/US098_COMB.pep:*
29: /EMC_Celerra_SIDS3/ptodata/2/paa/US099_COMB.pep:*
30: /EMC_Celerra_SIDS3/ptodata/2/paa/US100_COMB.pep:*
31: /EMC_Celerra_SIDS3/ptodata/2/paa/US101_COMB.pep:*
32: /EMC_Celerra_SIDS3/ptodata/2/paa/US102_COMB.pep:*
33: /EMC_Celerra_SIDS3/ptodata/2/paa/US103_COMB.pep:*
34: /EMC_Celerra_SIDS3/ptodata/2/paa/US104_COMB.pep:*
35: /EMC_Celerra_SIDS3/ptodata/2/paa/US105_COMB.pep:*
36: /EMC_Celerra_SIDS3/ptodata/2/paa/US106_COMB.pep:*
37: /EMC_Celerra_SIDS3/ptodata/2/paa/US107_COMB.pep:*
38: /EMC_Celerra_SIDS3/ptodata/2/paa/US108_COMB.pep:*
39: /EMC_Celerra_SIDS3/ptodata/2/paa/US109_COMB.pep:*
40: /EMC_Celerra_SIDS3/ptodata/2/paa/US110_COMB.pep:*
41: /EMC_Celerra_SIDS3/ptodata/2/paa/US111_COMB.pep:*
42: /EMC_Celerra_SIDS3/ptodata/2/paa/US112_COMB.pep:*
43: /EMC_Celerra_SIDS3/ptodata/2/paa/US113_COMB.pep:*
44: /EMC_Celerra_SIDS3/ptodata/2/paa/US114_COMB.pep:*
45: /EMC_Celerra_SIDS3/ptodata/2/paa/US600_COMB.pep:*
46: /EMC_Celerra_SIDS3/ptodata/2/paa/US601_COMB.pep:*
47: /EMC_Celerra_SIDS3/ptodata/2/paa/US602_COMB.pep:*
48: /EMC_Celerra_SIDS3/ptodata/2/paa/US603_COMB.pep:*
49: /EMC_Celerra_SIDS3/ptodata/2/paa/US604_COMB.pep:*
50: /EMC_Celerra_SIDS3/ptodata/2/paa/US605_COMB.pep:*
51: /EMC_Celerra_SIDS3/ptodata/2/paa/US606_COMB.pep:*
52: /EMC_Celerra_SIDS3/ptodata/2/paa/US607_COMB.pep:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	52	100.0	9	1	PCT-IL03-00501A-30	Sequence 30, Appl
2	52	100.0	9	1	PCT-US00-04326-8	Sequence 8, Appli
3	52	100.0	9	1	PCT-US00-25559-3	Sequence 3, Appli
4	52	100.0	9	1	PCT-US01-20182-23	Sequence 23, Appl
5	52	100.0	9	1	PCT-US03-16736-9	Sequence 9, Appli
6	52	100.0	9	1	PCT-US03-17641-20	Sequence 20, Appl
7	52	100.0	9	1	PCT-US03-30031A-10	Sequence 10, Appl
8	52	100.0	9	1	PCT-US04-04340-118	Sequence 118, App
9	52	100.0	9	1	PCT-US05-10597-1	Sequence 1, Appli
10	52	100.0	9	1	PCT-US98-01499-49	Sequence 49, Appl
11	52	100.0	9	1	PCT-US99-20344-16	Sequence 16, Appl
12	52	100.0	9	9	US-07-926-666-27	Sequence 27, Appl
13	52	100.0	9	10	US-08-027-746-49	Sequence 49, Appl
14	52	100.0	9	11	US-08-103-396A-54	Sequence 54, Appl
15	52	100.0	9	11	US-08-103-396A-549	Sequence 549, App
16	52	100.0	9	11	US-08-103-396A-634	Sequence 634, App

17	52	100.0	9	11	US-08-103-396A-657	Sequence 657, App
18	52	100.0	9	12	US-08-233-496A-2	Sequence 2, Appli
19	52	100.0	9	12	US-08-261-541A-1	Sequence 1, Appli
20	52	100.0	9	12	US-08-278-634-13	Sequence 13, Appl
21	52	100.0	9	13	US-08-315-961A-26	Sequence 26, Appl
22	52	100.0	9	13	US-08-344-824-18	Sequence 18, Appl
23	52	100.0	9	13	US-08-344-824A-18	Sequence 18, Appl
24	52	100.0	9	13	US-08-347-610-356	Sequence 356, App
25	52	100.0	9	13	US-08-347-610A-356	Sequence 356, App
26	52	100.0	9	13	US-08-347-610B-356	Sequence 356, App
27	52	100.0	9	13	US-08-347-610C-356	Sequence 356, App
28	52	100.0	9	13	US-08-354-679-12	Sequence 12, Appl
29	52	100.0	9	13	US-08-354-679B-12	Sequence 12, Appl
30	52	100.0	9	16	US-08-651-925-67	Sequence 67, Appl
31	52	100.0	9	16	US-08-651-925A-67	Sequence 67, Appl
32	52	100.0	9	18	US-08-815-631-2	Sequence 2, Appli
33	52	100.0	9	18	US-08-819-669-26	Sequence 26, Appl
34	52	100.0	9	18	US-08-819-669D-26	Sequence 26, Appl
35	52	100.0	9	18	US-08-819-669E-26	Sequence 26, Appl
36	52	100.0	9	18	US-08-820-360-1	Sequence 1, Appli
37	52	100.0	9	18	US-08-880-979-3	Sequence 3, Appli
38	52	100.0	9	19	US-08-922-869-12	Sequence 12, Appl
39	52	100.0	9	19	US-08-922-869A-12	Sequence 12, Appl
40	52	100.0	9	19	US-08-922-869B-12	Sequence 12, Appl
41	52	100.0	9	19	US-08-944-744-1	Sequence 1, Appli
42	52	100.0	9	19	US-08-992-124-1	Sequence 1, Appli
43	52	100.0	9	20	US-09-003-253-49	Sequence 49, Appl
44	52	100.0	9	20	US-09-049-850-6	Sequence 6, Appli
45	52	100.0	9	20	US-09-060-706-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

PCT-IL03-00501A-30

; Sequence 30, Application PC/TIL0300501A

; GENERAL INFORMATION:

; APPLICANT: GAVISH-GALILEE BIO APPLICATIONS LTD.

; APPLICANT: GROSS, Gideon

; APPLICANT: MARGALIT, Alon

; TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC

; TITLE OF INVENTION: PEPTIDE EPITOPES

; FILE REFERENCE: GAVISH-004 PCT

; CURRENT APPLICATION NUMBER: PCT/IL03/00501A

; CURRENT FILING DATE: 2003-06-12

; PRIOR APPLICATION NUMBER: US 60/388,273

; PRIOR FILING DATE: 2002-06-12

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 30

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

PCT-IL03-00501A-30

Query Match 100.0%; Score 52; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 2

PCT-US00-04326-8

; Sequence 8, Application PC/TUS0004326

; GENERAL INFORMATION:

; APPLICANT: Chiari, Rita

; APPLICANT: Coulie, Pierre G.

; APPLICANT: Boon-Falleur, Thierry

; TITLE OF INVENTION: TYROSINE KINASE RECEPTOR EphA3 ANTIGENIC PEPTIDES

; FILE REFERENCE: L0461/7057WO

; CURRENT APPLICATION NUMBER: PCT/US00/04326

; CURRENT FILING DATE: 2000-02-18

; EARLIER APPLICATION NUMBER: US 60/121,170

; EARLIER FILING DATE: 1999-02-22

; EARLIER APPLICATION NUMBER: US 60/158,566

; EARLIER FILING DATE: 1999-10-08

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US00-04326-8

Query Match 100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 3

PCT-US00-25559-3

; Sequence 3, Application PC/TUS0025559

; GENERAL INFORMATION:

; APPLICANT: Zycos Inc.

; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES

; FILE REFERENCE: 08191-013WO1

; CURRENT APPLICATION NUMBER: PCT/US00/25559

; CURRENT FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: PCT/US00/25559

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: US 60/169,846

; PRIOR FILING DATE: 1999-12-09

; PRIOR APPLICATION NUMBER: US 60/154,665

; PRIOR FILING DATE: 1999-09-16

; NUMBER OF SEQ ID NOS: 163

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US00-25559-3

Query Match 100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 4

PCT-US01-20182-23
; Sequence 23, Application PC/TUS0120182
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: PCT/US01/20182
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-20182-23

Query Match 100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 5

PCT-US03-16736-9
; Sequence 9, Application PC/TUS0316736
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484W00
; CURRENT APPLICATION NUMBER: PCT/US03/16736
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Synthetic Peptide
PCT-US03-16736-9

Query Match 100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 6

PCT-US03-17641-20

; Sequence 20, Application PC/TUS0317641

; GENERAL INFORMATION:

; APPLICANT: Bilsborough, Janine

; APPLICANT: Zhang, Yi

; APPLICANT: Schultz, Erwin

; APPLICANT: Panichelli, Christophe

; APPLICANT: Van der Bruggen, Pierre

; APPLICANT: Boon-Falleur, Thierry

; APPLICANT: Traversari, Catia

; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 and Cw16 Molecules And

; TITLE OF INVENTION: Thereof

; FILE REFERENCE: LUD-5756.1 PCT

; CURRENT APPLICATION NUMBER: PCT/US03/17641

; CURRENT FILING DATE: 2003-06-04

; PRIOR APPLICATION NUMBER: US 10/164,078

; PRIOR FILING DATE: 2002-06-05

; PRIOR APPLICATION NUMBER: US 10/164,121

; PRIOR FILING DATE: 2002-06/05

; NUMBER OF SEQ ID NOS: 37

; SEQ ID NO 20

; LENGTH: 9

; TYPE: PRT

; ORGANISM: H. sapiens

; FEATURE:

PCT-US03-17641-20

Query Match 100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 7

PCT-US03-30031A-10

; Sequence 10, Application PC/TUS0330031A

; GENERAL INFORMATION:

; APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH

; TITLE OF INVENTION: MAGE C2 ANTIGENIC PEPTIDES AND USES THEREOF

; FILE REFERENCE: LUD 5780.2 PCT

; CURRENT APPLICATION NUMBER: PCT/US03/30031A

; CURRENT FILING DATE: 2003-09-26

; PRIOR APPLICATION NUMBER: 60/413,844

; PRIOR FILING DATE: 2002-09-27

; PRIOR APPLICATION NUMBER: 60/433,983

; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/459,263
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-30031A-10

Query Match 100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 8

PCT-US04-04340-118
; Sequence 118, Application PC/TUS0404340
; GENERAL INFORMATION:
; APPLICANT: Antigenics, Inc.
; TITLE OF INVENTION: IMPROVED HEAT SHOCK PROTEIN-BASED VACCINES AND
; TITLE OF INVENTION: IMMUNOTHERAPIES
; FILE REFERENCE: 8449-405-228
; CURRENT APPLICATION NUMBER: PCT/US04/04340
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/503,417
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/463,746
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 60/462,469
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/447,142
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 118
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-04340-118

Query Match 100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 9

PCT-US05-10597-1
; Sequence 1, Application PC/TUS0510597
; GENERAL INFORMATION:
; APPLICANT: Cytomatrix, LLC
; APPLICANT: Pykett, Mark J.

```

; APPLICANT:  Rosenzweig, Michael
; TITLE OF INVENTION:  METHODS FOR PRODUCTION OF REGULATORY T CELLS AND USES THEREOF
; FILE REFERENCE:  C1005.70014WO00
; CURRENT APPLICATION NUMBER:  PCT/US05/10597
; CURRENT FILING DATE:  2005-03-29
; PRIOR APPLICATION NUMBER:  US 60/557,669
; PRIOR FILING DATE:  2004-03-29
; NUMBER OF SEQ ID NOS:  58
; SOFTWARE:  PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH:  9
;   TYPE:  PRT
;   ORGANISM:  Artificial sequence
;   FEATURE:
;   OTHER INFORMATION:  Homo sapiens source
PCT-US05-10597-1

```

```

Query Match          100.0%;  Score 52;  DB 1;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 7.7e+06;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

RESULT 10

PCT-US98-01499-49

```

; Sequence 49, Application PC/TUS9801499
; GENERAL INFORMATION:
;   APPLICANT:  Pangaea, Inc.
;   TITLE OF INVENTION:  MICROPARTICLES FOR DELIVERY
;   TITLE OF INVENTION:  OF NUCLEIC ACID
;   NUMBER OF SEQUENCES:  107
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Fish & Richardson, P.C.
;     STREET:  225 Franklin Street
;     CITY:  Boston
;     STATE:  MA
;     COUNTRY:  US
;     ZIP:  02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  Windows95
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US98/01499
;     FILING DATE:  22-JAN-1998
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/787,547
;     FILING DATE:  22-JAN-1997
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Fraser, Janis K.
;     REGISTRATION NUMBER:  34,819
;     REFERENCE/DOCKET NUMBER:  08191/003WO1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  617-542-5070
;     TELEFAX:  617-542-8906
;     TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  49:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US98-01499-49

Query Match 100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||||
Db 1 EADPTGHSY 9

RESULT 11
PCT-US99-20344-16
; Sequence 16, Application PC/TUS9920344
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; TITLE OF INVENTION: AN ANTIGENIC PEPTIDE ENCODED BY AN ALTERNATIVE OPEN READING FRA
; TITLE OF INVENTION: HUMAN MACROPHAGE COLONY-STIMULATING FACTOR
; FILE REFERENCE: L0461/7040WO
; CURRENT APPLICATION NUMBER: PCT/US99/20344
; CURRENT FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Window Version 3.0
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-20344-16

Query Match 100.0%; Score 52; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|||||||
Db 1 EADPTGHSY 9

RESULT 12
US-07-926-666-27
; Sequence 27, Application US/07926666
; GENERAL INFORMATION:
; APPLICANT: KUDO, RALPH T
; APPLICANT: GREY, HOWARD M
; APPLICANT: SETTE, ALESSANDRO
; APPLICANT: CELIS, ESTEBAN
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND KHOURIE AND CREW
; STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/926,666
; FILING DATE: 19920807
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BASTIAN, KEVIN L
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-50
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-926-666-27

```

```

Query Match          100.0%; Score 52; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 13
US-08-027-746-49
; Sequence 49, Application US/08027746
; GENERAL INFORMATION:
; APPLICANT: KUBO, Ralph T.
; APPLICANT: GREY, Howard M.
; APPLICANT: SETTE, Alessandro
; APPLICANT: CELIS, Esteban
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 249
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/027,746
; FILING DATE: 19930305
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774

```

; REFERENCE/DOCKET NUMBER: 14137-50-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-027-746-49

Query Match 100.0%; Score 52; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 14

US-08-103-396A-54

; Sequence 54, Application US/08103396A
; GENERAL INFORMATION:
; APPLICANT: KUBO, Ralph T.
; APPLICANT: GREY, Howard M.
; APPLICANT: SETTE, Alessandro
; APPLICANT: CELIS, Esteban
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 662
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/103,396A
; FILING DATE: 06-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-JUL-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-50-2

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-103-396A-54

```

```

Query Match          100.0%; Score 52; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

RESULT 15

US-08-103-396A-549

; Sequence 549, Application US/08103396A

; GENERAL INFORMATION:

```

; APPLICANT: KUBO, Ralph T.
; APPLICANT: GREY, Howard M.
; APPLICANT: SETTE, Alessandro
; APPLICANT: CELIS, Esteban
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 662
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1492

```

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/103,396A
; FILING DATE: 06-AUG-1993
; CLASSIFICATION: 424

```

; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-JUL-1992
; CLASSIFICATION: 424

```

; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; CLASSIFICATION: 424

```

; ATTORNEY/AGENT INFORMATION:

```

; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-50-2

```

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 549:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-103-396A-549

Query Match 100.0%; Score 52; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

Search completed: August 25, 2006, 01:11:18
Job time : 605 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e-26.rapn.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
---------------------------------	---	---------------------------------------	---------------------------	--

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-26.rapn.

[start](#)

[Go Back to previous pag](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2006, 01:01:22 ; Search time 40 Seconds
(without alignments)
19.416 Million cell updates/sec

Title: US-08-819-669E-26
Perfect score: 52
Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 361526 seqs, 86294087 residues

Total number of hits satisfying chosen parameters: 361526

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA New:*
1: /EMC_Celerra_SIDS3/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/paa/US11_NEW_COMB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
--------	------------

No.	Score	Match	Length	DB	ID	Description
1	52	100.0	9	6	US-10-362-715A-13	Sequence 13, Appl
2	52	100.0	9	6	US-10-497-088A-4	Sequence 4, Appli
3	52	100.0	9	6	US-10-447-161A-9	Sequence 9, Appli
4	52	100.0	9	7	US-11-375-226A-3	Sequence 3, Appli
5	52	100.0	309	6	US-10-657-022A-71	Sequence 71, Appl
6	52	100.0	445	5	US-09-601-565D-7	Sequence 7, Appli
7	52	100.0	446	5	US-09-601-565D-4	Sequence 4, Appli
8	52	100.0	1342	6	US-10-497-088A-14	Sequence 14, Appl
9	44	84.6	369	7	US-11-371-354-73367	Sequence 73367, A
10	43	82.7	315	7	US-11-371-354-69197	Sequence 69197, A
11	43	82.7	318	7	US-11-371-354-71659	Sequence 71659, A
12	42	80.8	319	7	US-11-371-354-73341	Sequence 73341, A
13	37	71.2	1049	6	US-10-669-920-860	Sequence 860, App
14	36	69.2	9	6	US-10-362-715A-12	Sequence 12, Appl
15	36	69.2	10	6	US-10-362-715A-23	Sequence 23, Appl
16	36	69.2	10	6	US-10-447-161A-25	Sequence 25, Appl
17	36	69.2	314	6	US-10-657-022A-73	Sequence 73, Appl
18	36	69.2	314	7	US-11-439-334-2	Sequence 2, Appli
19	36	69.2	314	7	US-11-371-354-69501	Sequence 69501, A
20	36	69.2	372	6	US-10-510-953-38	Sequence 38, Appl
21	36	69.2	389	7	US-11-442-668-23	Sequence 23, Appl
22	36	69.2	403	5	US-09-601-565D-5	Sequence 5, Appli
23	36	69.2	428	6	US-10-553-674-53	Sequence 53, Appl
24	36	69.2	450	5	US-09-601-565D-2	Sequence 2, Appli
25	36	69.2	453	5	US-09-601-565D-9	Sequence 9, Appli
26	36	69.2	599	7	US-11-442-668-59	Sequence 59, Appl
27	35	67.3	346	7	US-11-371-354-12740	Sequence 12740, A
28	35	67.3	346	7	US-11-371-354-65581	Sequence 65581, A
29	35	67.3	346	7	US-11-371-354-76818	Sequence 76818, A
30	35	67.3	359	1	PCT-US06-18535-8064	Sequence 8064, Ap
31	35	67.3	359	7	US-11-431-855-8064	Sequence 8064, Ap
32	35	67.3	561	8	US-60-836-986-30881	Sequence 30881, A
33	35	67.3	734	7	US-11-431-708-2503	Sequence 2503, Ap
34	35	67.3	734	7	US-11-475-062-6125	Sequence 6125, Ap
35	35	67.3	734	8	US-60-812-075-13	Sequence 13, Appl
36	35	67.3	873	7	US-11-431-708-2258	Sequence 2258, Ap
37	35	67.3	873	7	US-11-475-062-3172	Sequence 3172, Ap
38	35	67.3	873	8	US-60-819-940-70	Sequence 70, Appl
39	35	67.3	873	8	US-60-812-075-14	Sequence 14, Appl
40	35	67.3	925	7	US-11-431-708-2259	Sequence 2259, Ap
41	35	67.3	925	7	US-11-475-062-3173	Sequence 3173, Ap
42	35	67.3	925	8	US-60-812-075-15	Sequence 15, Appl
43	35	67.3	931	7	US-11-431-708-2261	Sequence 2261, Ap
44	35	67.3	931	7	US-11-475-062-3175	Sequence 3175, Ap
45	35	67.3	931	8	US-60-812-075-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-10-362-715A-13

; Sequence 13, Application US/10362715A

; GENERAL INFORMATION:

; APPLICANT: Schuler, Gerold

; APPLICANT: Schuler-Thurner, Beatrice

; TITLE OF INVENTION: METHOD FOR READY-TO-USE, ANTIGEN LOADED OR UNLOADED,

; TITLE OF INVENTION: CRYOCONSERVED MATURE DENDRITIC CELLS

; FILE REFERENCE: ARG015

; CURRENT APPLICATION NUMBER: US/10/362,715A
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09790
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 10041515.6
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-715A-13

Query Match 100.0%; Score 52; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 2

US-10-497-088A-4

; Sequence 4, Application US/10497088A
; GENERAL INFORMATION:
; APPLICANT: Germeraad, Wilfred
; APPLICANT: Logtenberg, Ton
; APPLICANT: Lekkerkerker, Annemarie N
; TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen
; TITLE OF INVENTION: presenting cell contacted with such conjugate, their use
; TITLE OF INVENTION: for vaccination or as medicament, and methods for their
; TITLE OF INVENTION: production or generation
; FILE REFERENCE: 0070 US 00 CON
; CURRENT APPLICATION NUMBER: US/10/497,088A
; CURRENT FILING DATE: 2005-06-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MAGE-1.A1 specific peptide
US-10-497-088A-4

Query Match 100.0%; Score 52; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 1 EADPTGHSY 9

RESULT 3

US-10-447-161A-9

; Sequence 9, Application US/10447161A
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong Fu

```

; TITLE OF INVENTION: MUTANT FIBRONECTIN AND TUMOR METASTASIS
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161A
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161A-9

```

```

Query Match          100.0%; Score 52; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 4
US-11-375-226A-3
; Sequence 3, Application US/11375226A
; GENERAL INFORMATION:
; APPLICANT: Yang, Yuh-Cheng
; APPLICANT: Tsao, Yeou-Ping
; APPLICANT: Chen, Show-Li
; TITLE OF INVENTION: A PEPTIDE ANTIGEN OF HUMAN PAPILLOMAVIRUS TYPE 16 AND APPLICATI
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 943371-IE1
; CURRENT APPLICATION NUMBER: US/11/375,226A
; CURRENT FILING DATE: 2006-03-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: melanoma antigen-1 peptide 161-169(negative control)
US-11-375-226A-3

```

```

Query Match          100.0%; Score 52; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+05;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EADPTGHSY 9

```

```

RESULT 5
US-10-657-022A-71
; Sequence 71, Application US/10657022A
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.

```

```
; APPLICANT:  Diamond, David C.
; APPLICANT:  Liu, Liping
; APPLICANT:  Liu, Zheng
; TITLE OF INVENTION:  EPI TOPE SEQUENCES
; FILE REFERENCE:  MANNK.032A
; CURRENT APPLICATION NUMBER:  US/10/657,022A
; CURRENT FILING DATE:  2003-09-05
; PRIOR APPLICATION NUMBER:  60/409,123
; PRIOR FILING DATE:  2002-09-06
; NUMBER OF SEQ ID NOS:  690
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 71
;   LENGTH:  309
;   TYPE:  PRT
;   ORGANISM:  Homo sapiens
US-10-657-022A-71
```

```
Query Match          100.0%;  Score 52;  DB 6;  Length 309;
Best Local Similarity 100.0%;  Pred. No. 0.035;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;
```

```
Qy      1 EADPTGHSY 9
        |||||
Db      161 EADPTGHSY 169
```

RESULT 6

US-09-601-565D-7

```
; Sequence 7, Application US/09601565D
; GENERAL INFORMATION:
; APPLICANT:  Smith Kline Beecham Biologicals
; TITLE OF INVENTION:  Processes for the Production of Therapeutic Compositions
; FILE REFERENCE:  B45126
; CURRENT APPLICATION NUMBER:  US/09/601,565D
; CURRENT FILING DATE:  2000-08-03
; NUMBER OF SEQ ID NOS:  15
; SOFTWARE:  PatentIn version 3.3
; SEQ ID NO 7
;   LENGTH:  445
;   TYPE:  PRT
;   ORGANISM:  Artificial
;   FEATURE:
;   OTHER INFORMATION:  Fusion protein of CLYTA-MAGE1-Histidine
US-09-601-565D-7
```

```
Query Match          100.0%;  Score 52;  DB 5;  Length 445;
Best Local Similarity 100.0%;  Pred. No. 0.052;
Matches      9;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;
```

```
Qy      1 EADPTGHSY 9
        |||||
Db      288 EADPTGHSY 296
```

RESULT 7

US-09-601-565D-4

```
; Sequence 4, Application US/09601565D
; GENERAL INFORMATION:
; APPLICANT:  Smith Kline Beecham Biologicals
; TITLE OF INVENTION:  Processes for the Production of Therapeutic Compositions
; FILE REFERENCE:  B45126
```

```

; CURRENT APPLICATION NUMBER: US/09/601,565D
; CURRENT FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fusion protein of LPD-MAGE1-Histidine
US-09-601-565D-4

```

```

Query Match          100.0%; Score 52; DB 5; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      289 EADPTGHSY 297

```

RESULT 8

```

US-10-497-088A-14
; Sequence 14, Application US/10497088A
; GENERAL INFORMATION:
; APPLICANT: Germeraad, Wilfred
; APPLICANT: Logtenberg, Ton
; APPLICANT: Lekkerkerker, Annemarie N
; TITLE OF INVENTION: Antigen presenting cell targeting conjugate, an antigen
; TITLE OF INVENTION: presenting cell contacted with such conjugate, their use
; TITLE OF INVENTION: for vaccination or as medicament, and methods for their
; TITLE OF INVENTION: production or generation
; FILE REFERENCE: 0070 US 00 CON
; CURRENT APPLICATION NUMBER: US/10/497,088A
; CURRENT FILING DATE: 2005-06-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 1342
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MatDC16-Cgamma4-MAGE-A1
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (836)..(836)
; OTHER INFORMATION: Unsure amino acid
US-10-497-088A-14

```

```

Query Match          100.0%; Score 52; DB 6; Length 1342;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      161 EADPTGHSY 169

```

RESULT 9

```

US-11-371-354-73367
; Sequence 73367, Application US/11371354

```

```

; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73367
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-73367

```

```

Query Match          84.6%; Score 44; DB 7; Length 369;
Best Local Similarity 77.8%; Pred. No. 1.4;
Matches      7; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        | | | | | :
Db      193 EVDPTGHSF 201

```

```

RESULT 10
US-11-371-354-69197
; Sequence 69197, Application US/11371354
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586

```

; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69197
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-69197

Query Match 82.7%; Score 43; DB 7; Length 315;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| || ||||
Db 167 EVDPAGHSY 175

RESULT 11

US-11-371-354-71659
; Sequence 71659, Application US/11371354
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 71659
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-71659

Query Match 82.7%; Score 43; DB 7; Length 318;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| || ||||
Db 171 EVDPAGHSY 179

RESULT 12

US-11-371-354-73341

; Sequence 73341, Application US/11371354

; GENERAL INFORMATION:

; APPLICANT: CARRINO, JOHN

; APPLICANT: LIANG, FENG

; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR

; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS

; FILE REFERENCE: INV-1005-UT2

; CURRENT APPLICATION NUMBER: US/11/371,354

; CURRENT FILING DATE: 2006-03-07

; PRIOR APPLICATION NUMBER: 60/673,045

; PRIOR FILING DATE: 2005-04-19

; PRIOR APPLICATION NUMBER: 60/665,199

; PRIOR FILING DATE: 2005-03-25

; PRIOR APPLICATION NUMBER: 60/665,200

; PRIOR FILING DATE: 2005-03-25

; PRIOR APPLICATION NUMBER: 60/659,493

; PRIOR FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: 60/659,492

; PRIOR FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: 60/953,586

; PRIOR FILING DATE: 2005-02-15

; PRIOR APPLICATION NUMBER: 60/651,390

; PRIOR FILING DATE: 2005-02-08

; NUMBER OF SEQ ID NOS: 78682

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 73341

; LENGTH: 319

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-371-354-73341

Query Match 80.8%; Score 42; DB 7; Length 319;

Best Local Similarity 77.8%; Pred. No. 2.9;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9

| | | | |

Db 171 EVDPTSHSY 179

RESULT 13

US-10-669-920-860

; Sequence 860, Application US/10669920

; GENERAL INFORMATION:

; APPLICANT: Morris, David W.

; APPLICANT: Malandro, Marc S.

; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER

; FILE REFERENCE: 20366-066001

; CURRENT APPLICATION NUMBER: US/10/669,920

; CURRENT FILING DATE: 2003-09-23

; PRIOR APPLICATION NUMBER: US 10/004,113

; PRIOR FILING DATE: 2001-10-23

; PRIOR APPLICATION NUMBER: US 10/052,482

; PRIOR FILING DATE: 2001-11-08

; PRIOR APPLICATION NUMBER: US 09/997,722

; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: US 10/034,650

; PRIOR FILING DATE: 2001-12-20

```

; PRIOR APPLICATION NUMBER: US 10/085,117
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 10/322,281
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 10/322,696
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 1441
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 860
;   LENGTH: 1049
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-669-920-860

```

```

Query Match          71.2%;   Score 37;   DB 6;   Length 1049;
Best Local Similarity 100.0%;   Pred. No. 91;
Matches      6;   Conservative      0;   Mismatches      0;   Indels      0;   Gaps      0;

```

```

Qy      4 PTGHSY 9
        |||||
Db      52 PTGHSY 57

```

RESULT 14

```

US-10-362-715A-12
; Sequence 12, Application US/10362715A
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: Schuler-Thurner, Beatrice
; TITLE OF INVENTION: METHOD FOR READY-TO-USE, ANTIGEN LOADED OR UNLOADED,
; TITLE OF INVENTION: CRYOCONSERVED MATURE DENDRITIC CELLS
; FILE REFERENCE: ARG015
; CURRENT APPLICATION NUMBER: US/10/362,715A
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09790
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 10041515.6
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-362-715A-12

```

```

Query Match          69.2%;   Score 36;   DB 6;   Length 9;
Best Local Similarity 66.7%;   Pred. No. 3.2e+05;
Matches      6;   Conservative      0;   Mismatches      3;   Indels      0;   Gaps      0;

```

```

Qy      1 EADPTGHSY 9
        |||||
Db      1 EVDPIGHLY 9

```

RESULT 15

```

US-10-362-715A-23
; Sequence 23, Application US/10362715A
; GENERAL INFORMATION:

```

```

; APPLICANT: Schuler, Gerold
; APPLICANT: Schuler-Thurner, Beatrice
; TITLE OF INVENTION: METHOD FOR READY-TO-USE, ANTIGEN LOADED OR UNLOADED,
; TITLE OF INVENTION: CRYOCONSERVED MATURE DENDRITIC CELLS
; FILE REFERENCE: ARG015
; CURRENT APPLICATION NUMBER: US/10/362,715A
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09790
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 10041515.6
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-715A-23

```

```

Query Match          69.2%; Score 36; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 1;
Matches      6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      1 EADPTGHSY 9
        | | | | |
Db      2 EVDPIGHLy 10

```

Search completed: August 25, 2006, 01:12:05
Job time : 41 secs

SCORE 1.3 BuildDate: 12/06/2005

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-81 start

A;Cross-references: UNIPROT:Q10635; UNIPARC:UPI000013A7EA; GB:Z73902; GB:AL123456; NID
 Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-J
 White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4
 Query Match 67.3%; Score 35; DB 2; Length 385; Best Local Similarity 66.7%; Pred. No. 60; Matc

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2006, 00:54:42 ; Search time 39 Seconds
 (without alignments)
 22.204 Million cell updates/sec

Title: US-08-819-669E-26
 Perfect score: 52
 Sequence: 1 EADPTGHSY 9

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	52	100.0	280	2	JC2358	melanoma antigen M
2	44	84.6	369	2	I38659	melanoma antigen M
3	43	82.7	234	2	I38667	melanoma antigen M

4	43	82.7	315	2	I38668	melanoma antigen M
5	42	80.8	319	2	I38660	melanoma antigen M
6	38	73.1	129	2	E72685	hypothetical prote
7	38	73.1	305	2	H83287	conserved hypothet
8	37	71.2	555	1	RGASWA	regulatory protein
9	36	69.2	133	2	I38663	melanoma antigen M
10	36	69.2	314	2	JC2360	melanoma antigen M
11	36	69.2	314	2	JC2361	melanoma antigen M
12	36	69.2	1375	2	T37672	probable DNA repai
13	36	69.2	3396	1	A42551	genome polyprotein
14	35	67.3	98	2	F70769	hypothetical prote
15	35	67.3	385	2	B87441	rod shape-determin
16	35	67.3	428	2	AD2938	hypothetical prote
17	35	67.3	430	2	C98344	sugar-binding prot
18	35	67.3	925	1	A39216	nucleotide diphosp
19	35	67.3	1033	2	S02168	type I site-specif
20	35	67.3	1187	2	T31351	endo-1,4-beta-xyla
21	34	65.4	197	2	A70832	hypothetical prote
22	34	65.4	215	2	T35768	hypothetical prote
23	34	65.4	224	2	T34937	hypothetical prote
24	34	65.4	322	2	AH1348	oligopeptide ABC t
25	34	65.4	370	2	S49008	fork head protein
26	34	65.4	497	1	S33938	penton protein (II
27	34	65.4	668	2	T18635	hypothetical prote
28	34	65.4	749	2	H82691	topoisomerase IV s
29	34	65.4	878	2	S44543	hypothetical prote
30	34	65.4	1184	2	T09484	cartilage intermed
31	34	65.4	1670	2	S71551	DNA-directed DNA p
32	34	65.4	3942	2	T42730	Bassoon protein -
33	33	63.5	214	2	AH0308	conserved hypothet
34	33	63.5	246	2	T51967	proteasome endopep
35	33	63.5	288	2	A56279	carbon-monoxide de
36	33	63.5	295	2	C69180	adhesion protein -
37	33	63.5	299	2	H82907	pseudouridine synt
38	33	63.5	301	2	C71194	hypothetical prote
39	33	63.5	341	2	T07148	G-box binding fact
40	33	63.5	372	2	S32581	lignin peroxidase
41	33	63.5	388	2	C90059	3-hydroxy-3-methyl
42	33	63.5	457	2	T39751	major facilitator
43	33	63.5	488	1	A53107	sulfite oxidase (E
44	33	63.5	488	1	S55874	sulfite oxidase (E
45	33	63.5	597	1	S37849	DNA intrastrand cr

ALIGNMENTS

RESULT 1

JC2358

melanoma antigen MAGE-1 - human

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Feb-2000

C;Accession: JC2358

R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.

Biochem. Biophys. Res. Commun. 202, 549-555, 1994

A;Title: Cloning and analysis of MAGE-1-related genes.

A;Reference number: JC2358; MUID:94311935; PMID:8037761

A;Accession: JC2358

A;Molecule type: mRNA

A;Residues: 1-280

A;Cross-references: UNIPARC:UPI0000178982

A;Experimental source: melanoma cell line DM150
C;Genetics:
A;Gene: MAGE
C;Superfamily: tumor associated protein MAGE
F;161-169/Region: HLA-A1 binding #status predicted

Query Match 100.0%; Score 52; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 161 EADPTGHSY 169

RESULT 2

I38659
melanoma antigen MAGE-10 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I38659
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.;
Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f
A;Reference number: I38659; MUID:95012457; PMID:7927540
A;Accession: I38659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-369
A;Cross-references: UNIPROT:P43363; UNIPARC:UPI0000000C57; EMBL:U10685; NID:g533510; P
C;Genetics:
A;Gene: GDB:MAGEA10; MAGE10
A;Cross-references: GDB:331126
A;Map position: Xq28-Xq28
A;Introns: #status absent
C;Superfamily: tumor associated protein MAGE

Query Match 84.6%; Score 44; DB 2; Length 369;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 193 EVDPTGHSF 201

RESULT 3

I38667
melanoma antigen MAGE-8 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I38667
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.;
Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f
A;Reference number: I38659; MUID:95012457; PMID:7927540
A;Accession: I38667
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-234
A;Cross-references: UNIPROT:P43361; UNIPARC:UPI00000335D6; EMBL:U10693; NID:g533525; P

C;Genetics:
A;Gene: GDB:MAGEA8; MAGE8
A;Cross-references: GDB:331123
A;Map position: Xq28-Xq28
A;Introns: #status absent
C;Superfamily: tumor associated protein MAGE

Query Match 82.7%; Score 43; DB 2; Length 234;
Best Local Similarity 77.8%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| || ||||
Db 171 EVDPAGHSY 179

RESULT 4

I38668

melanoma antigen MAGE-9 - human

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

C;Accession: I38668

R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Immunogenetics 40, 360-369, 1994

A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f

A;Reference number: I38659; MUID:95012457; PMID:7927540

A;Accession: I38668

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-315

A;Cross-references: UNIPROT:P43362; UNIPARC:UPI000012EB2B; EMBL:U10694; NID:g533527; P

C;Genetics:

A;Gene: GDB:MAGEA9; MAGE9

A;Cross-references: GDB:331125

A;Map position: Xp21.3-Xp21.3

A;Introns: #status absent

C;Superfamily: tumor associated protein MAGE

Query Match 82.7%; Score 43; DB 2; Length 315;
Best Local Similarity 77.8%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| || ||||
Db 167 EVDPAGHSY 175

RESULT 5

I38660

melanoma antigen MAGE-11 - human

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004

C;Accession: I38660

R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.; Immunogenetics 40, 360-369, 1994

A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f

A;Reference number: I38659; MUID:95012457; PMID:7927540

A;Accession: I38660

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-319

A;Cross-references: UNIPROT:P43364; UNIPARC:UPI0000000C62; EMBL:U10686; NID:g533512; P
C;Genetics:
A;Gene: GDB:MAGEA11; MAGE11
A;Cross-references: GDB:331128
A;Map position: Xq28-Xq28
A;Introns: #status absent
C;Superfamily: tumor associated protein MAGE

Query Match 80.8%; Score 42; DB 2; Length 319;
Best Local Similarity 77.8%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| ||| |||
Db 171 EVDPTSHSY 179

RESULT 6

E72685

hypothetical protein APE0901 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: E72685

R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tak
DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerop

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: E72685

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-129

A;Cross-references: UNIPROT:Q9YDL2; UNIPARC:UPI000005DD2A; DDBJ:AP000060; NID:g5104188

A;Experimental source: strain K1

C;Genetics:

A;Gene: APE0901

C;Superfamily: Aeropyrum pernix hypothetical protein APE0901

Query Match 73.1%; Score 38; DB 2; Length 129;
Best Local Similarity 85.7%; Pred. No. 4.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DPTGHSY 9
|| ||||
Db 115 DPAGHSY 121

RESULT 7

H83287

conserved hypothetical protein PA2875 [imported] - Pseudomonas aeruginosa (strain PA01

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: H83287

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: H83287

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-305

A;Cross-references: UNIPROT:Q9HZX1; UNIPARC:UPI00000C5857; GB:AE004713; GB:AE004091; N

A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2875
C;Superfamily: methanol dehydrogenase regulatory protein

Query Match 73.1%; Score 38; DB 2; Length 305;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGH 7
:|||||
Db 283 QADPTGH 289

RESULT 8

RGASWA
regulatory protein wetA - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A39665
R;Marshall, M.A.; Timberlake, W.E.
Mol. Cell. Biol. 11, 55-62, 1991
A;Title: Aspergillus nidulans wetA activates spore-specific gene expression.
A;Reference number: A39665; MUID:91094871; PMID:1986246
A;Accession: A39665
A;Molecule type: DNA
A;Residues: 1-555
A;Cross-references: UNIPROT:P22022; UNIPARC:UPI0000138EF8; GB:M60528; GB:M35758; NID:g
C;Comment: The products of the genes brlA, abaA, and wetA are required for activation
C;Genetics:
A;Gene: wetA
C;Superfamily: regulatory protein wetA
C;Keywords: transcription regulation

Query Match 71.2%; Score 37; DB 1; Length 555;
Best Local Similarity 87.5%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EADPTGHS 8
||| ||||
Db 109 EADATGHS 116

RESULT 9

I38663
melanoma antigen MAGE-5 - human (fragments)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C;Accession: I38663; I38664; PH1299; PH1300
R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.;
Immunogenetics 40, 360-369, 1994
A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f
A;Reference number: I38659; MUID:95012457; PMID:7927540
A;Accession: I38663
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-124
A;Cross-references: UNIPROT:P43359; UNIPARC:UPI000012EB2A; EMBL:U10689; NID:g533518; P
A;Experimental source: MAGE-5a antigen
A;Accession: I38664
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
 A;Residues: 1-124
 A;Cross-references: UNIPARC:UPI000012EB2A; EMBL:U10690; NID:g533520; PIDN:AAA68874.1;
 A;Experimental source: MAGE-5b antigen
 A;Note: these sequences seem to be incomplete with respect to other members of the sup
 R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pe
 J. Exp. Med. 176, 1453-1457, 1992
 A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolyt
 A;Reference number: PH1294; MUID:93018875; PMID:1402688
 A;Accession: PH1299
 A;Molecule type: DNA
 A;Residues: 125-133
 A;Cross-references: UNIPARC:UPI0000042533
 A;Experimental source: MAGE 5 protein
 A;Accession: PH1300
 A;Molecule type: DNA
 A;Residues: 125-133
 A;Cross-references: UNIPARC:UPI0000042533
 A;Experimental source: MAGE 51 protein
 C;Genetics:
 A;Gene: GDB:MAGEA5; MAGE5
 A;Cross-references: GDB:331120
 A;Map position: Xq28-Xq28
 A;Introns: #status absent
 C;Superfamily: tumor associated protein MAGE

Query Match 69.2%; Score 36; DB 2; Length 133;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EADPTGHSY 9
 ||||| ::|
 Db 125 EADPTSNTY 133

RESULT 10
 JC2360
 melanoma antigen MAGE-6 - human
 N;Alternate names: tumor-associated antigen, MAGE-3b
 C;Species: Homo sapiens (man)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: JC2360; PH1301; I38665; G01445
 R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
 Biochem. Biophys. Res. Commun. 202, 549-555, 1994
 A;Title: Cloning and analysis of MAGE-1-related genes.
 A;Reference number: JC2358; MUID:94311935; PMID:8037761
 A;Accession: JC2360
 A;Molecule type: mRNA
 A;Residues: 1-314
 A;Cross-references: UNIPROT:P43360; UNIPARC:UPI000000D9B0
 A;Experimental source: melanoma cell line DM150
 R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pe
 J. Exp. Med. 176, 1453-1457, 1992
 A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolyt
 A;Reference number: PH1294; MUID:93018875; PMID:1402688
 A;Accession: PH1301
 A;Molecule type: DNA
 A;Residues: 168-176
 A;Cross-references: UNIPARC:UPI0000042625
 R;De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J.J.; Szikora, J.P.; De Smet, C.;
 Immunogenetics 40, 360-369, 1994

A;Title: Structure, chromosomal localization, and expression of 12 genes of the MAGE f
 A;Reference number: I38659; MUID:95012457; PMID:7927540
 A;Accession: I38665
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-314
 A;Cross-references: UNIPARC:UPI000000D9B0; EMBL:U10691; NID:g533522; PIDN:AAA68875.1;
 R;Fenton, R.G.
 submitted to the EMBL Data Library, June 1994
 A;Reference number: G07126
 A;Accession: G01445
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-314
 A;Cross-references: UNIPARC:UPI000000D9B0; EMBL:U10339; NID:g499121; PIDN:AAA19006.1;
 C;Genetics:
 A;Gene: GDB:MAGEA6; MAGE6
 A;Cross-references: GDB:331121
 A;Map position: Xq28-Xq28
 A;Introns: #status absent
 C;Superfamily: tumor associated protein MAGE
 F;168-176/Region: HLA-A1 binding #status predicted

Query Match 69.2%; Score 36; DB 2; Length 314;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EADPTGHSY 9
 | || || |
 Db 168 EVDPIGHVY 176

RESULT 11

JC2361

melanoma antigen MAGE-3 - human

N;Alternate names: MAGE 3 protein

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: JC2361; PH1296; I38438

R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.

Biochem. Biophys. Res. Commun. 202, 549-555, 1994

A;Title: Cloning and analysis of MAGE-1-related genes.

A;Reference number: JC2358; MUID:94311935; PMID:8037761

A;Accession: JC2361

A;Molecule type: mRNA

A;Residues: 1-314

A;Cross-references: UNIPROT:P43357; UNIPARC:UPI0000062194

A;Experimental source: melanoma cell line DM150

R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pe J. Exp. Med. 176, 1453-1457, 1992

A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolyt

A;Reference number: PH1294; MUID:93018875; PMID:1402688

A;Accession: PH1296

A;Molecule type: DNA

A;Residues: 168-176

A;Cross-references: UNIPARC:UPI000002F152

R;Gaugler, B.; Van den Eynde, B.; van der Bruggen, P.; Romero, P.; Gaforio, J.J.; De P J. Exp. Med. 179, 921-930, 1994

A;Title: Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous

A;Reference number: I38438; MUID:94157413; PMID:8113684

A;Accession: I38438

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-314
A;Cross-references: UNIPARC:UPI0000062194; EMBL:U03735; NID:g468825; PIDN:AAA17446.1;
C;Genetics:
A;Gene: MAGE-3
C;Superfamily: tumor associated protein MAGE
F;168-176/Region: HLA-A1 binding #status predicted

Query Match 69.2%; Score 36; DB 2; Length 314;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| || || |
Db 168 EVDPIGHLy 176

RESULT 12

T37672

probable DNA repair protein - fission yeast (*Schizosaccharomyces pombe*)
C;Species: *Schizosaccharomyces pombe*
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37672
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.
submitted to the EMBL Data Library, October 1999
A;Reference number: Z21736
A;Accession: T37672
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1375
A;Cross-references: UNIPROT:Q9UTL9; UNIPARC:UPI0000069886; EMBL:AL132675; PIDN:CAB5968
A;Experimental source: strain 972h-; cosmid c144
C;Genetics:
A;Gene: SPDB:SPAC144.05
A;Map position: 1
A;Introns: 1108/1; 1196/3; 1263/2; 1277/1
F;1088-1135/Domain: RING finger homology

Query Match 69.2%; Score 36; DB 2; Length 1375;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
|:|||| |
Db 810 ESDPTGDEY 818

RESULT 13

A42551

genome polyprotein - dengue virus type 1 (strain Singapore S275/90)
N;Contains: capsid protein; envelope protein; membrane protein; nonstructural protein
C;Species: dengue virus type 1
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C;Accession: A42551
R;Fu, J.; Tan, B.H.; Yap, E.H.; Chan, Y.C.; Tan, Y.H.
Virology 188, 953-958, 1992
A;Title: Full-length cDNA sequence of dengue type 1 virus (Singapore strain S275/90).
A;Reference number: A42551; MUID:92263809; PMID:1585663
A;Accession: A42551
A;Molecule type: genomic RNA

A;Residues: 1-3396
 A;Cross-references: UNIPROT:P33478; UNIPARC:UPI000002F845; GB:M87512
 C;Superfamily: hepatitis C virus genome polyprotein
 C;Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein
 F;1-114/Product: capsid protein #status predicted
 F;115-281/Product: membrane protein precursor #status predicted
 F;115-204/Domain: nonterminal signal sequence #status predicted
 F;205-281/Product: membrane protein #status predicted
 F;267-279/Domain: transmembrane #status predicted
 F;282-774/Product: envelope protein #status predicted
 F;753-769/Domain: transmembrane #status predicted
 F;775-1127/Product: nonstructural protein NS1 #status predicted
 F;1128-1344/Product: nonstructural protein NS2a #status predicted
 F;1345-1474/Product: nonstructural protein NS2b #status predicted
 F;1475-2093/Product: nonstructural protein NS3 #status predicted
 F;1668-1675/Region: nucleotide-binding motif A (P-loop)
 F;1755-1760/Region: nucleotide-binding motif B
 F;1759-1762/Region: DEAH motif
 F;2094-2243/Product: nonstructural protein NS4a #status predicted
 F;2244-2492/Product: nonstructural protein NS4b #status predicted
 F;2493-3396/Product: nonstructural protein NS5 #status predicted
 F;183,347,433/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 69.2%; Score 36; DB 1; Length 3396;
 Best Local Similarity 75.0%; Pred. No. 4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EADPTGHS 8
 . |:|| |||
 Db 3383 ESDPKGHS 3390

RESULT 14
 F70769
 hypothetical protein Rv1322 - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C;Accession: F70769
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
 Nature 393, 537-544, 1998
 A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: F70769
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-98

5	43	82.7	315	2	Q7Z5K4_HUMAN	Q7z5k4	homo sapien
6	43	82.7	318	2	Q9BUN9_HUMAN	Q9bun9	homo sapien
7	42	80.8	319	1	MAGAB_HUMAN	P43364	homo sapien
8	42	80.8	394	2	Q6ZRZ5_HUMAN	Q6zrz5	homo sapien
9	42	80.8	429	2	Q5ETU4_HUMAN	Q5etu4	homo sapien
10	40	76.9	259	1	PYRK_BACAN	Q81wf3	bacillus an
11	40	76.9	259	1	PYRK_BACCR	Q819s4	bacillus ce
12	40	76.9	259	2	Q3ENC9_BACTI	Q3enc9	bacillus th
13	40	76.9	259	2	Q4MJ43_BACCE	Q4mj43	bacillus ce
14	40	76.9	259	2	Q636E1_BACCZ	Q636e1	bacillus ce
15	40	76.9	259	2	Q6HES9_BACHK	Q6hes9	bacillus th
16	40	76.9	259	2	Q732I4_BACCL	Q732i4	bacillus ce
17	40	76.9	5094	2	Q2IZL4_RHOPA	Q2izl4	rhodopseudo
18	39	75.0	652	2	Q7SDF4_NEUCR	Q7sdf4	neurospora
19	39	75.0	1429	2	Q6CH67_YARLI	Q6ch67	yarrowia li
20	38	73.1	129	2	Q9YDL2_AERPE	Q9ydl2	aeropyrum p
21	38	73.1	130	2	Q825J6_STRAW	Q825j6	streptomyce
22	38	73.1	294	2	Q40M96_DESAC	Q40m96	desulfuromo
23	38	73.1	305	2	Q9HZX1_PSEAE	Q9hzx1	pseudomonas
24	38	73.1	337	2	Q4HXP0_GIBZE	Q4hxp0	gibberella
25	38	73.1	346	2	Q7RXH4_NEUCR	Q7rxh4	neurospora
26	38	73.1	355	2	Q475K8_RALEJ	Q475k8	ralstonia e
27	38	73.1	356	2	Q43QJ8_SOLUS	Q43qj8	solibacter
28	38	73.1	1001	2	Q4PBD5_USTMA	Q4pbd5	ustilago ma
29	38	73.1	1034	2	Q55XT8_CRYNE	Q55xt8	cryptococcu
30	38	73.1	1065	2	Q4PC22_USTMA	Q4pc22	ustilago ma
31	38	73.1	1085	2	Q755J0_ASHGO	Q755j0	ashbya goss
32	37	71.2	86	2	Q61989_MOUSE	Q61989	mus musculu
33	37	71.2	125	2	Q4L989_STAHJ	Q4l989	staphylococ
34	37	71.2	247	2	Q67RX7_SYMTH	Q67rx7	symbiobacte
35	37	71.2	249	2	Q5V7C7_HALMA	Q5v7c7	haloarcula
36	37	71.2	271	2	Q6MHS7_BDEBA	Q6mhs7	bdellovibri
37	37	71.2	279	2	Q3W747_9ACTO	Q3w747	frankia sp.
38	37	71.2	345	2	Q89L61_BRAJA	Q89l61	bradyrhizob
39	37	71.2	479	2	Q4NIV6_9MICC	Q4niv6	arthrobacte
40	37	71.2	555	1	WETA_EMENI	P22022	emericella
41	37	71.2	555	2	Q5BBZ3_EMENI	Q5bbz3	aspergillus
42	37	71.2	604	2	Q3U1F2_MOUSE	Q3ulf2	mus musculu
43	37	71.2	604	2	Q8BQ25_MOUSE	Q8bq25	mus musculu
44	37	71.2	622	1	PFA3_NEUCR	Q7s7c5	neurospora
45	37	71.2	642	2	Q3U0V9_MOUSE	Q3u0v9	mus musculu

ALIGNMENTS

RESULT 1

MAGA1_HUMAN

ID MAGA1_HUMAN STANDARD; PRT; 309 AA.
AC P43355; O00346;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 44.
DE Melanoma-associated antigen 1 (MAGE-1 antigen) (Antigen MZ2-E).
GN Name=MAGEA1; Synonyms=MAGE1, MAGE1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92086861; PubMed=1840703;
RA van der Bruggen P., Traversari C., Chomez P., Lurquin C., de Plaen E.,
RA van den Eynde B., Knuth A., Boon T.;
RT "A gene encoding an antigen recognized by cytolytic T lymphocytes on a
RT human melanoma.";
RL Science 254:1643-1647(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=94311935; PubMed=8037761;
RA Ding M., Beck R.J., Keller C.J., Fenton R.G.;
RT "Cloning and analysis of MAGE-1-related genes.";
RL Biochem. Biophys. Res. Commun. 202:549-555(1994).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=20314869; PubMed=10854409; DOI=10.1101/gr.10.6.758;
RA Mallon A.-M., Platzer M., Bate R., Gloeckner G., Botcherby M.R.M.,
RA Nordsiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D.,
RA Straw R.N.A., Weston P., Gilbert M., Fernando S., Goodall K.,
RA Hunter G., Greystrom J.S., Clarke D., Kimberley C., Goerdes M.,
RA Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W.,
RA Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A.,
RA Brown S.D.M.;
RT "Comparative genome sequence analysis of the Bpa/Str region in mouse
RT and man.";
RL Genome Res. 10:758-775(2000).
RN [4]
RP NUCLEOTIDE SEQUENCE, AND VARIANT ALA-32.
RA Chen H., Wang L., Mei M., Qin L., Cong X., Xu J., Wei L., Wang Y.,
RA Chen W.;
RT "The polymorphism of MAGE-1 gene in Chinese people.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-32.
RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ALA-32.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP MUTAGENESIS.
 RC TISSUE=Blood;
 RX MEDLINE=94157413; PubMed=8113684; DOI=10.1084/jem.179.3.921;
 RA Gaugler B., van den Eynde B., van der Bruggen P., Romero P.,
 RA Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.;
 RT "Human gene MAGE-3 codes for an antigen recognized on a melanoma by
 RT autologous cytolytic T lymphocytes."
 RL J. Exp. Med. 179:921-930(1994).
 RN [8]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=95012905; PubMed=7927954;
 RA Schultz-Thater E., Juretic A., Dellabona P., Luscher U., Siegrist W.,
 RA Harder F., Heberer M., Zuber M., Spagnoli G.C.;
 RT "MAGE-1 gene product is a cytoplasmic protein."
 RL Int. J. Cancer 59:435-439(1994).
 CC -!- FUNCTION: Not known, though may play a role in embryonal
 CC development and tumor transformation or aspects of tumor
 CC progression. Antigen recognized on a melanoma by autologous
 CC cytolytic T lymphocytes.
 CC -!- SUBCELLULAR LOCATION: Cytoplasm.
 CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
 CC such as melanoma, head and neck squamous cell carcinoma, lung
 CC carcinoma and breast carcinoma, but not in normal tissues except
 CC for testes. Never expressed in kidney tumors, leukemias and
 CC lymphomas.
 CC -!- SIMILARITY: Contains 1 MAGE domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; M77481; AAA03229.1; -; Unassigned_DNA.
 DR EMBL; U82670; -; NOT_ANNOTATED_CDS; Genomic_DNA.
 DR EMBL; AY148486; AAN62752.1; -; mRNA.
 DR EMBL; BT009789; AAP88791.1; -; mRNA.
 DR EMBL; BC017555; AAH17555.1; -; mRNA.
 DR PDB; 1W72; X-ray; C/F=161-169.
 DR Ensembl; ENSG00000126977; Homo sapiens.
 DR H-InvDB; HIX0017126; -.
 DR HGNC; HGNC:6796; MAGEA1.
 DR MIM; 300016; gene.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR InterPro; IPR002190; MAGE.
 DR PANTHER; PTHR11736; MAGE; 1.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS50838; MAGE; 1.
 KW 3D-structure; Antigen; Polymorphism; Tumor antigen.
 FT CHAIN 1 309 Melanoma-associated antigen 1.
 FT /FTId=PRO_0000156701.
 FT DOMAIN 102 301 MAGE.
 FT COMBIAS 33 36 Poly-Ser.
 FT VARIANT 32 32 T -> A (probable polymorphism).
 FT /FTId=VAR_004283.
 FT VARIANT 72 72 R -> Q (in dbSNP:2008144).
 FT /FTId=VAR_011737.
 FT MUTAGEN 163 163 D->A: Abolishes HLA-A1 binding.
 FT MUTAGEN 169 169 Y->A: Abolishes HLA-A1 binding.

SQ SEQUENCE 309 AA; 34342 MW; 544EEB1F9F4E9D33 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| | | | | | | |
Db 161 EADPTGHSY 169

RESULT 2

MAGAA_HUMAN

ID MAGAA_HUMAN STANDARD; PRT; 369 AA.
AC P43363;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 39.
DE Melanoma-associated antigen 10 (MAGE-10 antigen).
GN Name=MAGEA10; Synonyms=MAGE10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
RT the MAGE family."
RL Immunogenetics 40:360-369(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression.

CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
 CC such as melanoma, head and neck squamous cell carcinoma, lung
 CC carcinoma and breast carcinoma, but not in normal tissues except
 CC for testes and placenta.
 CC -!- SIMILARITY: Contains 1 MAGE domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; U10685; AAA68869.1; -; Genomic_DNA.
 DR EMBL; BC004105; AAH04105.1; -; mRNA.
 DR PIR; I38659; I38659.
 DR Ensembl; ENSG00000124260; Homo sapiens.
 DR H-InvDB; HIX0017116; -.
 DR HGNC; HGNC:6797; MAGEA10.
 DR MIM; 300343; gene.
 DR LinkHub; P43363; -.
 DR InterPro; IPR002190; MAGE.
 DR PANTHER; PTHR11736; MAGE; 2.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS50838; MAGE; 1.
 KW Antigen; Polymorphism; Tumor antigen.
 FT CHAIN 1 369 Melanoma-associated antigen 10.
 FT /FTid=PRO_0000156709.
 FT DOMAIN 134 333 MAGE.
 FT COMPBIAS 54 62 Poly-Ser.
 FT VARIANT 166 166 K -> R (in dbSNP:210585).
 FT /FTid=VAR_024528.
 SQ SEQUENCE 369 AA; 40767 MW; 16FA3301CAB716A6 CRC64;

Query Match 84.6%; Score 44; DB 1; Length 369;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 | |||||:
 Db 193 EVDPTGHSF 201

RESULT 3

MAGA8_HUMAN

ID MAGA8_HUMAN STANDARD; PRT; 234 AA.
 AC P43361;
 DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
 DT 01-NOV-1995, sequence version 1.
 DT 07-FEB-2006, entry version 32.
 DE Melanoma-associated antigen 8 (MAGE-8 antigen).
 GN Name=MAGEA8; Synonyms=MAGE8;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX MEDLINE=95012457; PubMed=7927540;
 RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
 RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
 RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
 RT "Structure, chromosomal localization, and expression of 12 genes of
 RT the MAGE family.";

```

RL   Immunogenetics 40:360-369(1994).
CC   -!- FUNCTION: Not known, though may play a role in embryonal
CC       development and tumor transformation or aspects of tumor
CC       progression.
CC   -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC       such as melanoma, head and neck squamous cell carcinoma, lung
CC       carcinoma and breast carcinoma, but not in normal tissues except
CC       for testes and placenta.
CC   -!- SIMILARITY: Contains 1 MAGE domain.
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; U10693; AAA68876.1; -; Genomic_DNA.
DR   PIR; I38667; I38667.
DR   Ensembl; ENSG00000156009; Homo sapiens.
DR   HGNC; HGNC:6806; MAGEA8.
DR   MIM; 300341; gene.
DR   InterPro; IPR002190; MAGE.
DR   PANTHER; PTHR11736; MAGE; 1.
DR   Pfam; PF01454; MAGE; 1.
DR   PROSITE; PS50838; MAGE; 1.
KW   Antigen; Tumor antigen.
FT   CHAIN           1      234      Melanoma-associated antigen 8.
FT                                     /FTid=PRO_0000156707.
FT   DOMAIN          112     234     MAGE.
FT   COMPIAS         40      43      Poly-Ser.
SQ   SEQUENCE        234 AA;  25197 MW;  058A92EE6003A982 CRC64;

Query Match           82.7%;  Score 43;  DB 1;  Length 234;
Best Local Similarity  77.8%;  Pred. No. 11;
Matches      7;  Conservative    0;  Mismatches    2;  Indels      0;  Gaps      0;

QY      1 EADPTGHSY 9
      | || |||
Db      171 EVDPAGHSY 179

```

RESULT 4

MAGA9_HUMAN

```

ID   MAGA9_HUMAN      STANDARD;          PRT;   315 AA.
AC   P43362; Q92910;
DT   01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1995, sequence version 1.
DT   07-FEB-2006, entry version 37.
DE   Melanoma-associated antigen 9 (MAGE-9 antigen).
GN   Name=MAGEA9; Synonyms=MAGE9;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=95012457; PubMed=7927540;
RA   de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA   de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA   Brasseur R., Chomez P., de Backer O., Cavenne W., Boon T.;
RT   "Structure, chromosomal localization, and expression of 12 genes of
RT   the MAGE family.";
RL   Immunogenetics 40:360-369(1994).

```

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Timms K.M., Bondeson M.L., Ansari-Lari M.A., Lagerstedt K.,
 RA Nelson D.L., Pettersson U., Gibbs R.A.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Not known, though may play a role in embryonal
 CC development and tumor transformation or aspects of tumor
 CC progression.
 CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
 CC such as melanoma, head and neck squamous cell carcinoma, lung
 CC carcinoma and breast carcinoma, but not in normal tissues except
 CC for testes and placenta.
 CC -!- SIMILARITY: Contains 1 MAGE domain.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; U10694; AAA68877.1; -; Genomic_DNA.
 DR EMBL; U66083; AAB67888.1; -; Genomic_DNA.
 DR EMBL; BC002351; AAH02351.1; -; mRNA.
 DR PIR; I38668; I38668.
 DR H-InvDB; HIX0017105; -.
 DR HGNC; HGNC:6807; MAGEA9.
 DR MIM; 300342; gene.
 DR InterPro; IPR002190; MAGE.
 DR PANTHER; PTHR11736; MAGE; 1.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS50838; MAGE; 1.
 KW Antigen; Tumor antigen.
 FT CHAIN 1 315 Melanoma-associated antigen 9.
 FT /FTId=PRO_0000156708.
 FT DOMAIN 108 307 MAGE.
 FT COMBIAS 34 37 Poly-Glu.
 FT COMBIAS 87 90 Poly-Glu.
 SQ SEQUENCE 315 AA; 35088 MW; 7FD2ED10D680D928 CRC64;

Query Match 82.7%; Score 43; DB 1; Length 315;

Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| || ||||
Db 167 EVDPAGHSY 175

RESULT 5

Q7Z5K4_HUMAN
ID Q7Z5K4_HUMAN PRELIMINARY; PRT; 315 AA.
AC Q7Z5K4;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Melanoma antigen family A 9 (Fragment).
GN Name=MAGEA9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Zhu J., Feng Z., Guan X.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY310325; AAP82171.1; -; mRNA.
DR InterPro; IPR002190; MAGE.
DR PANTHER; PTHR11736; MAGE; 1.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
FT NON_TER 315 315
SQ SEQUENCE 315 AA; 35116 MW; C9488470D409B96F CRC64;

Query Match 82.7%; Score 43; DB 2; Length 315;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
| || ||||
Db 167 EVDPAGHSY 175

RESULT 6

Q9BUN9_HUMAN
ID Q9BUN9_HUMAN PRELIMINARY; PRT; 318 AA.
AC Q9BUN9;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Melanoma antigen family A, 8.
GN Name=MAGEA8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skin;
 RG NIH MGC Project;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
 RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
 RA Phelan M., Farmer A.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skin;
 RA Director MGC Project;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; BC002455; AAH02455.1; -; mRNA.
 DR EMBL; BT007340; AAP36004.1; -; mRNA.
 DR EMBL; BC012744; AAH12744.1; -; mRNA.
 DR Ensembl; ENSG00000156009; Homo sapiens.
 DR InterPro; IPR002190; MAGE.
 DR PANTHER; PTHR11736; MAGE; 1.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS50838; MAGE; 1.
 SQ SEQUENCE 318 AA; 35215 MW; EA02C1FB42F6C080 CRC64;

 Query Match 82.7%; Score 43; DB 2; Length 318;
 Best Local Similarity 77.8%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EADPTGHSY 9
 | || ||||

RESULT 7

MAGAB_HUMAN

ID MAGAB_HUMAN STANDARD; PRT; 319 AA.
AC P43364;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-FEB-2006, entry version 36.
DE Melanoma-associated antigen 11 (MAGE-11 antigen).
GN Name=MAGEA11; Synonyms=MAGE11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
RT the MAGE family.";
RL Immunogenetics 40:360-369(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Not known, though may play a role in embryonal
CC development and tumor transformation or aspects of tumor
CC progression.
CC -!- INTERACTION:
CC Q96AJ1:CLUAP1; NbExp=1; IntAct=EBI-739552, EBI-739780;
CC Q96C88:SH2D4A; NbExp=1; IntAct=EBI-739552, EBI-747035;
CC Q15560:TCEA2; NbExp=1; IntAct=EBI-739552, EBI-710310;
CC -!- TISSUE SPECIFICITY: Expressed in many tumors of several types,
CC such as melanoma, head and neck squamous cell carcinoma, lung
CC carcinoma and breast carcinoma, but not in normal tissues except
CC for testes and placenta.

```

CC  -!- SIMILARITY: Contains 1 MAGE domain.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC  Distributed under the Creative Commons Attribution-NoDerivs License
CC  -----
DR  EMBL; U10686; AAA68870.1; -; Genomic_DNA.
DR  EMBL; BC004479; AAH04479.1; -; mRNA.
DR  PIR; I38660; I38660.
DR  IntAct; P43364; -.
DR  Ensembl; ENSG00000185247; Homo sapiens.
DR  H-InvDB; HIX0022316; -.
DR  HGNC; HGNC:6798; MAGEA11.
DR  MIM; 300344; gene.
DR  InterPro; IPR002190; MAGE.
DR  PANTHER; PTHR11736; MAGE; 1.
DR  Pfam; PF01454; MAGE; 1.
DR  PROSITE; PS50838; MAGE; 1.
KW  Antigen; Tumor antigen.
FT  CHAIN           1       319       Melanoma-associated antigen 11.
FT                                     /FTId=PRO_0000156710.
FT  DOMAIN          112      311      MAGE.
SQ  SEQUENCE        319 AA;  35536 MW;  F51A0B4140277BE3 CRC64;

Query Match           80.8%;  Score 42;  DB 1;  Length 319;
Best Local Similarity  77.8%;  Pred. No. 24;
Matches      7;  Conservative      0;  Mismatches      2;  Indels      0;  Gaps      0;

Qy          1 EADPTGHSY 9
             | ||| |||
Db          171 EVDPTSHSY 179

```

```

RESULT 8
Q6ZRZ5_HUMAN
ID  Q6ZRZ5_HUMAN  PRELIMINARY;  PRT;  394 AA.
AC  Q6ZRZ5;
DT  05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT  05-JUL-2004, sequence version 1.
DT  21-FEB-2006, entry version 8.
DE  CDNA FLJ45952 fis, clone PLACE7009563, highly similar to Melanoma-
DE  associated antigen 11.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC  Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Placenta;
RA  Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA  Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA  Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA  Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA  Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA  Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA  Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA  Isogai T.;
RT  "NEDO human cDNA sequencing project.";
RL  Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC  -----
CC  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms

```

CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AK127849; BAC87161.1; -; mRNA.
 DR Ensembl; ENSG00000185247; Homo sapiens.
 DR LinkHub; Q6ZRZ5; -.
 DR InterPro; IPR002190; MAGE.
 DR PANTHER; PTHR11736; MAGE; 1.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS50838; MAGE; 1.
 SQ SEQUENCE 394 AA; 44276 MW; 36D7A81D8749D896 CRC64;

Query Match 80.8%; Score 42; DB 2; Length 394;
 Best Local Similarity 77.8%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 | ||| |||
 Db 246 EVDPTSHSY 254

RESULT 9
 Q5ETU4_HUMAN
 ID Q5ETU4_HUMAN PRELIMINARY; PRT; 429 AA.
 AC Q5ETU4;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 4.
 DE Melanoma antigen family A 11.
 GN Name=MAGEA11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RX PubMed=15684378; DOI=10.1128/MCB.25.4.1238-1257.2005;
 RA Bai S., He B., Wilson E.M.;
 RT "Melanoma Antigen Gene Protein MAGE-11 Regulates Androgen Receptor
 RT Function by Modulating the Interdomain Interaction."
 RL Mol. Cell. Biol. 25:1238-1257(2005).

CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY747607; AAW71787.1; -; mRNA.
 DR Ensembl; ENSG00000185247; Homo sapiens.
 DR InterPro; IPR002190; MAGE.
 DR PANTHER; PTHR11736; MAGE; 1.
 DR Pfam; PF01454; MAGE; 1.
 DR PROSITE; PS50838; MAGE; 1.
 SQ SEQUENCE 429 AA; 48129 MW; FB399ABF47B4C49B CRC64;

Query Match 80.8%; Score 42; DB 2; Length 429;
 Best Local Similarity 77.8%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 | ||| |||
 Db 281 EVDPTSHSY 289

RESULT 10
 PYRK_BACAN
 ID PYRK_BACAN STANDARD; PRT; 259 AA.
 AC Q81WF3; Q6HUK1; Q6KNT6;
 DT 14-NOV-2003, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-2003, sequence version 1.
 DT 07-MAR-2006, entry version 27.
 DE Dihydroorotate dehydrogenase electron transfer subunit.
 GN Name=pyrK; OrderedLocusNames=BA4024, GBAA4024, BAS3736;
 OS *Bacillus anthracis*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC *Bacillus cereus* group.
 OX NCBI_TaxID=1392;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Ames / isolate Porton;
 RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
 RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
 RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
 RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
 RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
 RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
 RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
 RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
 RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
 RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
 RA Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
 RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
 RT "The genome sequence of *Bacillus anthracis* Ames and comparison to
 RT closely related bacteria.";
 RL Nature 423:81-86(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Ames ancestor;
 RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
 RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
 RA Fraser C.M.;
 RT "Bacillus anthracis comparative genomics.";
 RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Sterne;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of *Bacillus anthracis* Sterne.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Is responsible for channelling the electrons from the
 CC oxidation of dihydroorotate from the FMN redox center in the pyrD
 CC subunit to the ultimate electron acceptor NAD(+) (By similarity).
 CC -!- COFACTOR: Binds 1 2Fe-2S cluster per subunit (By similarity).
 CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
 CC -!- PATHWAY: Nucleotide biosynthesis; UMP biosynthesis; UMP from
 CC HCO(3)(-): step 4.
 CC -!- PATHWAY: Context: Pyrimidine biosynthesis.
 CC -!- SUBUNIT: Heterotetramer of 2 pyrK and 2 pyrD subunits (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the pyrK family.
 CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AE016879; AAP27751.1; -; Genomic_DNA.
 DR EMBL; AE017334; AAT33141.1; -; Genomic_DNA.
 DR EMBL; AE017225; AAT56038.1; -; Genomic_DNA.
 DR HSSP; P56968; 1EP3.
 DR GenomeReviews; AE016879_GR; BA4024.
 DR GenomeReviews; AE017225_GR; BAS3736.
 DR GenomeReviews; AE017334_GR; GBAA4024.
 DR TIGR; BA4024; -.
 DR TIGR; GBAA4024; -.
 DR HAMAP; MF_01211; -; 1.
 DR InterPro; IPR006058; 2Fe2S_fd_BS.
 DR InterPro; IPR012165; Cyc3_hyd_g.
 DR InterPro; IPR008333; Oxred_FAD_bd.
 DR InterPro; IPR001433; Oxred_FAD_NAD_bd.
 DR InterPro; IPR000951; Ph_dOase_redase.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PIRSF; PIRSF006816; Cyc3_hyd_g; 1.
 DR PRINTS; PR00409; PHDIOXRDTASE.
 KW 2Fe-2S; Complete proteome; Electron transport; FAD; Flavoprotein;
 KW Iron; Iron-sulfur; Metal-binding; Pyrimidine biosynthesis; Transport.
 FT CHAIN 1 259 Dihydroorotate dehydrogenase electron
 FT transfer subunit.
 FT /FTId=PRO_0000148353.
 FT METAL 221 221 Iron-sulfur (2Fe-2S) (By similarity).
 FT METAL 226 226 Iron-sulfur (2Fe-2S) (By similarity).
 FT METAL 229 229 Iron-sulfur (2Fe-2S) (By similarity).
 FT METAL 246 246 Iron-sulfur (2Fe-2S) (By similarity).
 SQ SEQUENCE 259 AA; 28439 MW; DC2768827E220805 CRC64;

Query Match 76.9%; Score 40; DB 1; Length 259;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 : ||:||||
 Db 234 QEDPSGHSY 242

RESULT 11
 PYRK_BACCR
 ID PYRK_BACCR STANDARD; PRT; 259 AA.
 AC Q819S4;
 DT 14-NOV-2003, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-2003, sequence version 1.
 DT 07-MAR-2006, entry version 24.
 DE Dihydroorotate dehydrogenase electron transfer subunit.
 GN Name=pyrK; OrderedLocusNames=BC3885;
 OS Bacillus cereus (strain ATCC 14579 / DSM 31).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=226900;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
 RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
 RA Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
 RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,

RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
 RA Overbeek R., Kyrpides N.C.;
 RT "Genome sequence of Bacillus cereus and comparative analysis with
 RT Bacillus anthracis.";
 RL Nature 423:87-91(2003).
 CC -!- FUNCTION: Is responsible for channelling the electrons from the
 CC oxidation of dihydroorotate from the FMN redox center in the pyrD
 CC subunit to the ultimate electron acceptor NAD(+) (By similarity).
 CC -!- COFACTOR: Binds 1 2Fe-2S cluster per subunit (By similarity).
 CC -!- COFACTOR: Binds 1 FAD per subunit (By similarity).
 CC -!- PATHWAY: Nucleotide biosynthesis; UMP biosynthesis; UMP from
 CC HCO(3)(-): step 4.
 CC -!- PATHWAY: Context: Pyrimidine biosynthesis.
 CC -!- SUBUNIT: Heterotetramer of 2 pyrK and 2 pyrD subunits (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the pyrK family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AE016877; AAP10806.1; -; Genomic_DNA.
 DR HSSP; P56968; 1EP3.
 DR GenomeReviews; AE016877_GR; BC3885.
 DR BioCyc; BCER226900:BC3885-MONOMER; -.
 DR HAMAP; MF_01211; -; 1.
 DR InterPro; IPR006058; 2Fe2S_fd_BS.
 DR InterPro; IPR012165; Cyc3_hyd_g.
 DR InterPro; IPR008333; Oxred_FAD_bd.
 DR InterPro; IPR001433; Oxred_FAD_NAD_bd.
 DR InterPro; IPR000951; Ph_dOase_redase.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PIRSF; PIRSF006816; Cyc3_hyd_g; 1.
 DR PRINTS; PR00409; PHDIOXRDTASE.
 KW 2Fe-2S; Complete proteome; Electron transport; FAD; Flavoprotein;
 KW Iron; Iron-sulfur; Metal-binding; Pyrimidine biosynthesis; Transport.
 FT CHAIN 1 259 Dihydroorotate dehydrogenase electron
 FT transfer subunit.
 FT /FTId=PRO_0000148354.
 FT METAL 221 221 Iron-sulfur (2Fe-2S) (By similarity).
 FT METAL 226 226 Iron-sulfur (2Fe-2S) (By similarity).
 FT METAL 229 229 Iron-sulfur (2Fe-2S) (By similarity).
 FT METAL 246 246 Iron-sulfur (2Fe-2S) (By similarity).
 SQ SEQUENCE 259 AA; 28416 MW; D8F893A27E25919B CRC64;

 Query Match 76.9%; Score 40; DB 1; Length 259;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 1 EADPTGHSY 9
 : ||:||||
 Db 234 QEDPSGHSY 242

RESULT 12
 Q3ENC9_BACTI
 ID Q3ENC9_BACTI PRELIMINARY; PRT; 259 AA.
 AC Q3ENC9;
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 08-NOV-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.

```

DE   Dihydroorotate dehydrogenase electron transfer subunit (EC 1.3.3.1).
GN   ORFNames=RBTH_02089;
OS   Bacillus thuringiensis serovar israelensis ATCC 35646.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC   Bacillus cereus group.
OX   NCBI_TaxID=339854;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 35646;
RA   Anderson I., Sorokin A., Kapatral V., Reznik G., Bhattacharya A.,
RA   Mikhailova N., Burd H., Joukov V., Kaznadzey D., Walunas T.,
RA   D'Souza M., Larsen N., Pusch G., Liolios K., Grechkin Y., Lapidus A.,
RA   Goltsman E., Chu L., Fonstein M., Ehrlich D., Overbeek R.,
RA   Kyrpides N., Ivanova N.;
RT   "Comparative genome analysis of Bacillus cereus group genomes with
RT   Bacillus subtilis.";
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; AAJM01000353; EAO52817.1; -; Genomic_DNA.
DR   GO; GO:0004158; F:dihydroorotate oxidase activity; IEA.
DR   GO; GO:0050660; F:FAD binding; IEA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   GO; GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA.
DR   InterPro; IPR012165; Cyc3_hyd_g.
DR   InterPro; IPR008333; Oxred_FAD_bd.
DR   InterPro; IPR001433; Oxred_FAD_NAD_bd.
DR   InterPro; IPR000951; Ph_dOase_redase.
DR   Pfam; PF00970; FAD_binding_6; 1.
DR   Pfam; PF00175; NAD_binding_1; 1.
DR   PIRSF; PIRSF006816; Cyc3_hyd_g; 1.
DR   PRINTS; PR00409; PHDIOXRDTASE.
KW   Oxidoreductase.
SQ   SEQUENCE   259 AA;  28444 MW;  E39A55E165134782 CRC64;

Query Match          76.9%;  Score 40;  DB 2;  Length 259;
Best Local Similarity 66.7%;  Pred. No. 47;
Matches      6;  Conservative      2;  Mismatches      1;  Indels      0;  Gaps      0;

QY      1 EADPTGHSY 9
      : ||:||||
Db      234 QEDPSGHSY 242

RESULT 13
Q4MJ43_BACCE
ID   Q4MJ43_BACCE   PRELIMINARY;   PRT;   259 AA.
AC   Q4MJ43;
DT   02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT   02-AUG-2005, sequence version 1.
DT   07-FEB-2006, entry version 2.
DE   Dihydroorotate dehydrogenase electron transfer subunit.
GN   Name=pyrDII; ORFNames=BCE_G9241_3870;
OS   Bacillus cereus G9241.

```

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=269801;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=G9241;
 RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
 RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
 RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
 RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
 RA Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
 RA Popovic T., Fraser C.M.;
 RT "Identification of anthrax toxin genes in a Bacillus cereus associated
 RT with an illness resembling inhalation anthrax."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AAEK01000049; EAL12213.1; -; Genomic_DNA.
 DR GO; GO:0050660; F:FAD binding; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA.
 DR InterPro; IPR012165; Cyc3_hyd_g.
 DR InterPro; IPR000951; Ph_dOase_redase.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PIRSF; PIRSF006816; Cyc3_hyd_g; 1.
 DR PRINTS; PR00409; PHDIOXRDTASE.
 SQ SEQUENCE 259 AA; 28421 MW; DDE1B379910A3D10 CRC64;

 Query Match 76.9%; Score 40; DB 2; Length 259;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 Qy 1 EADPTGHSY 9
 : ||:||||
 Db 234 QEDPSGHSY 242

RESULT 14
 Q636E1_BACCZ
 ID Q636E1_BACCZ PRELIMINARY; PRT; 259 AA.
 AC Q636E1;
 DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 25-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Dihydroorotate dehydrogenase, electron transfer subunit (EC 1.3.3.1).
 GN Name=pyrK; OrderedLocusNames=BCE33L3644;
 OS Bacillus cereus (strain ZK / E33L).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=288681;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,

RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of *Bacillus cereus* ZK.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; CP000001; AAU16622.1; -; Genomic_DNA.
 DR GO; GO:0004158; F:dihydroorotate oxidase activity; IEA.
 DR GO; GO:0050660; F:FAD binding; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA.
 DR InterPro; IPR012165; Cyc3_hyd_g.
 DR InterPro; IPR008333; Oxred_FAD_bd.
 DR InterPro; IPR001433; Oxred_FAD_NAD_bd.
 DR InterPro; IPR000951; Ph_dOase_redase.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PIRSF; PIRSF006816; Cyc3_hyd_g; 1.
 DR PRINTS; PR00409; PHDIOXRDTASE.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 259 AA; 28439 MW; DC2768827E220805 CRC64;

Query Match 76.9%; Score 40; DB 2; Length 259;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EADPTGHSY 9
 : ||:||||
 Db 234 QEDPSGHSY 242

RESULT 15
 Q6HES9_BACHK
 ID Q6HES9_BACHK PRELIMINARY; PRT; 259 AA.
 AC Q6HES9;
 DT 19-JUL-2004, integrated into UniProtKB/TreMBL.
 DT 19-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 11.
 DE Dihydroorotate dehydrogenase, electron transfer subunit (EC 1.3.3.1).
 GN Name=pyrK; OrderedLocusNames=BT9727_3627;
 OS *Bacillus thuringiensis* subsp. *konkukian*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*;
 OC *Bacillus cereus* group.
 OX NCBI_TaxID=180856;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=97-27;
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of *Bacillus thuringiensis* 97-27.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AE017355; AAT60634.1; -; Genomic_DNA.

DR GO; GO:0004158; F:dihydroorotate oxidase activity; IEA.
 DR GO; GO:0050660; F:FAD binding; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006221; P:pyrimidine nucleotide biosynthesis; IEA.
 DR InterPro; IPR012165; Cyc3_hyd_g.
 DR InterPro; IPR008333; Oxred_FAD_bd.
 DR InterPro; IPR001433; Oxred_FAD_NAD_bd.
 DR InterPro; IPR000951; Ph_dOase_redase.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00175; NAD_binding_1; 1.
 DR PIRSF; PIRSF006816; Cyc3_hyd_g; 1.
 DR PRINTS; PR00409; PHDIOXRDTASE.
 KW Complete proteome; Oxidoreductase.
 SQ SEQUENCE 259 AA; 28439 MW; DC2768827E220805 CRC64;

Query Match 76.9%; Score 40; DB 2; Length 259;
 Best Local Similarity 66.7%; Pred. No. 47;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EADPTGHSY 9
 : ||:||||
 Db 234 QEDPSGHSY 242

Search completed: August 25, 2006, 00:59:28
 Job time : 302 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e-8.rge.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
---------------------------------	---	---------------------------------------	---------------------------	--

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-8.rge.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 09:08:38 ; Search time 30844 Seconds
(without alignments)
11763.639 Million cell updates/sec

Title: US-08-819-669E-8
Perfect score: 5674
Sequence: 1 CCCGGGGCACCCTGGCATC.....TAATGATCTGGGTGGATCC 5674

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	5674	100.0	5674	2	AR060975	AR060975 Sequence
	2	5674	100.0	5674	2	AR153499	AR153499 Sequence
	3	5674	100.0	5674	2	I24013	I24013 Sequence 1
	4	5674	100.0	5674	2	I36923	I36923 Sequence 8
	5	5674	100.0	5674	2	AR268060	AR268060 Sequence
	6	5674	100.0	5674	2	AR322041	AR322041 Sequence
	7	5674	100.0	5674	2	AR361125	AR361125 Sequence
	8	5674	100.0	5674	2	AR721150	AR721150 Sequence
c	9	5567.8	98.1	88597	5	AC152005	AC152005 Homo sapi
c	10	5535.8	97.6	40359	5	AC153070	AC153070 Homo sapi
c	11	2763.2	48.7	169351	5	AC116666	AC116666 Homo sapi
c	12	2763.2	48.7	173962	5	AF274856	AF274856 Homo sapi
	13	2655	46.8	11495	2	AR167373	AR167373 Sequence
	14	2655	46.8	11495	5	HSU10687	U10687 Human MAGE-
	15	2654.8	46.8	161664	5	U82696	U82696 Homo sapien
	16	2654.8	46.8	200395	5	AF274855	AF274855 Homo sapi
	17	2513.6	44.3	4895	2	AR167374	AR167374 Sequence
	18	2513.6	44.3	4895	2	AX658231	AX658231 Sequence
	19	2513.6	44.3	4895	5	HSU10688	U10688 Human MAGE-
	20	2429.6	42.8	4736	2	AR167376	AR167376 Sequence
	21	2429.6	42.8	4736	5	HSU10690	U10690 Human MAGE-
	22	2422.8	42.7	4741	2	AR167375	AR167375 Sequence
	23	2422.8	42.7	4741	2	AX658171	AX658171 Sequence
	24	2422.8	42.7	4741	5	HSU10689	U10689 Human MAGE-
	25	2419	42.6	2419	2	AR153498	AR153498 Sequence
	26	2419	42.6	2419	2	I36922	I36922 Sequence 7
	27	2419	42.6	2419	2	AR268059	AR268059 Sequence
	28	2419	42.6	2419	2	AR322040	AR322040 Sequence
	29	2419	42.6	2419	2	AR361124	AR361124 Sequence
	30	2419	42.6	2419	2	AR721149	AR721149 Sequence
	31	2408	42.4	2420	2	AR007331	AR007331 Sequence
	32	2408	42.4	2420	2	AR167368	AR167368 Sequence
	33	2408	42.4	2420	2	CQ977089	CQ977089 Sequence
	34	2408	42.4	2420	2	DD161424	DD161424 EPITOPE S
	35	2408	42.4	2420	2	AR236284	AR236284 Sequence
	36	2408	42.4	2420	2	AX658175	AX658175 Sequence
	37	2408	42.4	2420	5	HUMMAG1A	M77481 Human antig
c	38	2405.8	42.4	204030	12	AC146919	AC146919 Pongo pyg
c	39	2405.8	42.4	234364	12	AC148185	AC148185 Pongo pyg
	40	2404.2	42.4	204030	12	AC146919	AC146919 Pongo pyg
	41	2404.2	42.4	234364	12	AC148185	AC148185 Pongo pyg
c	42	2353	41.5	164994	12	AC148183	AC148183 Macaca mu
c	43	2353	41.5	168595	12	AC146354	AC146354 Macaca mu
	44	2328	41.0	178515	12	AC009621	AC009621 Homo sapi
	45	2313.4	40.8	181915	5	AC145689	AC145689 Pan trogl

ALIGNMENTS

RESULT 1
AR060975

LOCUS AR060975 5674 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 1 from patent US 5843448.
 ACCESSION AR060975
 VERSION AR060975.1 GI:5988666
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 5674)
 AUTHORS Chen,Y.-T., Stockert,E., Chen,Y., Garin-Chesa,P., Rettig,W.J. and Old,L.J.
 TITLE Tumor rejection antigen precursor
 JOURNAL Patent: US 5843448-A 1 01-DEC-1998;
 FEATURES Location/Qualifiers
 source 1. .5674
 /organism="unknown"
 /mol_type="unassigned DNA"
 ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db    181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
      |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
      |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
      |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
      |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
      |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCAATCCAACCCCCA 600
      |||
  
```

Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCCACCACATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCCACCACATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCCACCCCCACGCCCCTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCCACCCCCACGCCCCTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Qy	1321	CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500

Qy	1501	ATCCACTGAGGGGAGTGGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCCAAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCCAAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACTACCCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACTACCCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400

Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGCTGCGCAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGCTGCGCAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTTGGATTTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTTGGATTTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360

Db	3301	 CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260

Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160

```

Qy      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA 5220
        |||
Db      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA 5220

Qy      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280
        |||
Db      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280

Qy      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
        |||
Db      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340

Qy      5341 TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCAGTCTGAGCA 5400
        |||
Db      5341 TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCAGTCTGAGCA 5400

Qy      5401 TCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
        |||
Db      5401 TCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460

Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
        |||
Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520

Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTTGGGGCTCCGGGTGAGAGTG 5580
        |||
Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTTGGGGCTCCGGGTGAGAGTG 5580

Qy      5581 GTGGAGTGTCATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
        |||
Db      5581 GTGGAGTGTCATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        |||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 2

AR153499

LOCUS AR153499 5674 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 8 from patent US 6235525.

ACCESSION AR153499

VERSION AR153499.1 GI:15121031

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 5674)

AUTHORS van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.

TITLE Isolated nucleic acid molecules coding for tumor rejection antigen precursor MAGE-3 and uses thereof

JOURNAL Patent: US 6235525-A 8 22-MAY-2001;

FEATURES Location/Qualifiers

source 1. .5674

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;

Best Local Similarity 100.0%; Pred. No. 0;

		Matches	5674;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	CCCCGGG	CACCACTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC	60							
Db	1	CCCCGGG	CACCACTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC	60							
Qy	61	ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG	120								
Db	61	ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG	120								
Qy	121	CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180								
Db	121	CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180								
Qy	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240								
Db	181	TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240								
Qy	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300								
Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300								
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360								
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360								
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420								
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420								
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480								
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480								
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540								
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540								
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600								
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600								
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCATCCGCCAGCCATTCCACCCT	660								
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCATCCGCCAGCCATTCCACCCT	660								
Qy	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720								
Db	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720								
Qy	721	CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780								
Db	721	CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780								
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840								
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840								
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900								
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900								

Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800

Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCACATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCACATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760

Db	2701	 TCACCCAGGATGTGGCTTCTTTTTCCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	 CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	 GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCAGAG	2940
Db	2881	 GACCAGAACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	 AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	 ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	 CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	 GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	 GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	 ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	 CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGATTCCCT	3420
Db	3361	 GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	 CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	 ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	 GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660

Db	3601	TCAGTCCTGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGCCA	4380
Db	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCACCGCCA	4380
Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560

Qy	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTGAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTGAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAAGTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAAGTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460

```

Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
        |||
Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520

Qy      5521 CTCCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
        |||
Db      5521 CTCCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580

Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
        |||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        |||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 3

I24013

LOCUS I24013 5674 bp DNA linear PAT 07-OCT-1996

DEFINITION Sequence 1 from patent US 5541104.

ACCESSION I24013

VERSION I24013.1 GI:1603883

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 5674)

AUTHORS Chen,Y.-T., Stockert,E., Chen,Y., Garin-Chesa,P., Rettig,W.J., van der Bruggen,P., Boon-Falleur,T. and Old,L.J.

TITLE Monoclonal antibodies which bind to tumor rejection antigen precursor mage-1

JOURNAL Patent: US 5541104-A 1 30-JUL-1996;

FEATURES Location/Qualifiers

source 1. .5674

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy      61 ATCCAAACATCTTCACGCTCACCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db      61 ATCCAAACATCTTCACGCTCACCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy      121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db      121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy      181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db      181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy      241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        |||

```

Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCAATCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCAATCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCCACCCCCACGCCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCCACCCCCACGCCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200

Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCAGAGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCAGAGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCTAGGACACCGCACCCCTGTCTGAG	2100

Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCACTAGAGGGAGCGTCCCAGGCC	3060

Db	3001	 ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	 CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	 GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Db	3181	 GTCCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCAG	3240
Qy	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	 ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	 CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCT	3420
Db	3361	 GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	 CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	 ACAGAGCAGAGGATGCACAGGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	 GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCCTCTCACTTCCT	3660
Db	3601	 TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	 CCTTCAGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCACTTCTC	3780
Db	3721	 GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	 AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	 CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960

Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961		4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021		4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081		4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141		4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201		4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Db	4261		4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321		4380
Qy	4381	CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381		4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441		4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501		4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561		4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621		4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681		4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741		4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801		4860

Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATA	5460
Db	5401	TCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATA	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT	5640
Qy	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674
Db	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674

RESULT 4

I36923

LOCUS

I36923

5674 bp

DNA

linear

PAT 13-MAY-1997

DEFINITION Sequence 8 from patent US 5612201.
 ACCESSION I36923
 VERSION I36923.1 GI:2084883
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 5674)
 AUTHORS De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J.-P., De Smet,C.
 and Chomez,P.
 TITLE Isolated nucleic acid molecules useful in determining expression of
 a tumor rejection antigen precursor
 JOURNAL Patent: US 5612201-A 8 18-MAR-1997;
 FEATURES Location/Qualifiers
 source 1. .5674
 /organism="unknown"
 /mol_type="unassigned DNA"
 ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
        |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
        |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
        |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
        |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
        |||
  
```

Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCACCCACGCCCCACTCCACCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCACCCACGCCCCACTCCACCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500

Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400

Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTTGGATTTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTTGGATTTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360

Db	3301		CAGAGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361		GTAGCACTGAGAAGCCAGGGCTGTGCTTGC GGCTGCACCCTGAGGGCCGTGGATTCTCT	3420
Db	3361		GTAGCACTGAGAAGCCAGGGCTGTGCTTGC GGCTGCACCCTGAGGGCCGTGGATTCTCT	3420
Qy	3421		CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421		CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481		ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481		ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541		GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541		GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601		TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCTCT	3660
Db	3601		TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCTCT	3660
Qy	3661		CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661		CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721		GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721		GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961		TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961		TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021		CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTCCCACTAC	4080
Db	4021		CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTCCCACTAC	4080
Qy	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141		GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141		GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260

Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCAATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160

```

Qy      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA 5220
        |||
Db      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA 5220

Qy      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280
        |||
Db      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280

Qy      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
        |||
Db      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340

Qy      5341 TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTTCTTCTCCATGCAGTCTGAGCA 5400
        |||
Db      5341 TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTTCTTCTCCATGCAGTCTGAGCA 5400

Qy      5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC 5460
        |||
Db      5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC 5460

Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
        |||
Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520

Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
        |||
Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580

Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
        |||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        |||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 5

AR268060

LOCUS AR268060 5674 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 8 from patent US 6498021.

ACCESSION AR268060

VERSION AR268060.1 GI:29698299

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 5674)

AUTHORS Guagler,B.

TITLE Isolated nucleic acid molecules coding for tumor rejection antigen precursor MAGe-8 and uses thereof

JOURNAL Patent: US 6498021-A 8 24-DEC-2002;
Ludwig Institute for Cancer Research; New York, NY

FEATURES Location/Qualifiers

source 1..5674

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
      |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
      |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
      |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
      |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
      |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
      |||
Db    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Qy    601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT 660
      |||
Db    601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT 660

Qy    661 CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCTCG 720
      |||
Db    661 CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCTCG 720

Qy    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTTGTGGGGCAGAGA 780
      |||
Db    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTTGTGGGGCAGAGA 780

Qy    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840
      |||
Db    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840

Qy    841 CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA 900
      |||
```

Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800

Qy	1801	ACCCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTCAGCCCTGGACACC	2700

Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGAAGTCAAGTACAGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGAAGTCAAGTACAGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGCTGCGGAGGTCCTTCGTTATCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGCTGCGGAGGTCCTTCGTTATCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTTCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660

Db	3601		TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661		CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661		CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721		GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721		GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Qy	3781		AGCTGAGGCCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781		AGCTGAGGCCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961		TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961		TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021		CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021		CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141		GCCAAGCACCTCTTGATATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141		GCCAAGCACCTCTTGATATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261		AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261		AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321		CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321		CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381		CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381		CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501		CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560

Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCTGCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATAC	5460

```

Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
        |||
Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520

Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
        |||
Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580

Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
        |||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        |||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 6

AR322041

LOCUS AR322041 5674 bp DNA linear PAT 17-AUG-2003

DEFINITION Sequence 8 from patent US 6565857.

ACCESSION AR322041

VERSION AR322041.1 GI:33707547

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 5674)

AUTHORS van den Eynde,B., van den Bruggen,P. and Boon-Falleur,T.

TITLE Methods for treating a disorder by using Mage-3 or Mage-3 related materials

JOURNAL Patent: US 6565857-A 8 20-MAY-2003;

Ludwig Institute for Cancer Research; New York, NY

FEATURES Location/Qualifiers

source 1. .5674

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy      61 ATCCAAACATCTTCACGCTCACCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
        |||
Db      61 ATCCAAACATCTTCACGCTCACCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy      121 CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db      121 CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy      181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db      181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy      241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

```

Db	241		300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301		360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361		420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421		480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481		540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541		600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Db	601		660
Qy	661	CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Db	661		720
Qy	721	CCAGGAAACATCCGGGTGCCCCGATGTGACGCCACTGACTTGCGCATTTGTGGGGCAGAGA	780
Db	721		780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781		840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841		900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901		960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTTC	1020
Db	961		1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021		1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081		1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCACCCCATTCGCATTCCCATCCCCACCCAACC	1200

Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCTCAGAGGACCCAGCACCTAGGACACCGCACCCCTGTCTGAG	2100

Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000

Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCTGGTGTG	3960

Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGGGCACCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGGGCACCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCACTCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCACTCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCATGGGGAGCCCAGGAAGCTGCTCACCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTT	4860

Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAGTGAAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAGTGAAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCCTTCT	5640
Qy	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674
Db	5641	GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674

RESULT 7
AR361125

LOCUS AR361125 5674 bp DNA linear PAT 17-AUG-2003
 DEFINITION Sequence 8 from patent US 6599699.
 ACCESSION AR361125
 VERSION AR361125.1 GI:33768828
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 5674)
 AUTHORS Guagler,B., Van den Eynde,B., van den Bruggen,P. and Boon-Falleur,T.
 TITLE Methods for diagnosing a disorder by assaying for MAGE-3
 JOURNAL Patent: US 6599699-A 8 29-JUL-2003;
 Ludwig Institute for Cancer Research; New York, NY
 FEATURES Location/Qualifiers
 source 1. .5674
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
      |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
      |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
      |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
      |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
      |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCA 600
  
```

Db	541		CCCCACTCCAATGCTCACTCCCCTGACCCAACCCCTCTTCATTGTCATTCCAACCCCA	600
Qy	601		CCCCACATCCCCACCCCATCCCTCAACCTGATGCCCATCCGCCCAGCCATTCCACCCT	660
Db	601		CCCCACATCCCCACCCCATCCCTCAACCTGATGCCCATCCGCCCAGCCATTCCACCCT	660
Qy	661		CACCCCCACCCCAACCCCAACGCCCCTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Db	661		CACCCCCACCCCAACCCCAACGCCCCTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Qy	721		CCAGGAAACATCCGGGTGCCCCGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721		CCAGGAAACATCCGGGTGCCCCGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781		GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781		GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901		GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGAAGA	960
Db	901		GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGAAGA	960
Qy	961		CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961		CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGGCC	1140
Db	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGGCC	1140
Qy	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201		CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201		CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Db	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCCTCACTGCCCCAAC	1320
Qy	1321		CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAAATCC	1380
Db	1321		CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAAATCC	1380
Qy	1381		GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381		GGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441		TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAG	1500

Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400

Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300

Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Db	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTCCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTCCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260

Db	4201	 TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Db	4261	 AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	 CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCTTGCTGGGTGATAATCA	4440
Db	4381	 CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCTTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	 GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	 CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAA	4620
Db	4561	 GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	 GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	 CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	 GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	 GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Db	4861	 CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	 GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	 TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	 TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160

```

Db      5101 TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT 5160
Qy      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA 5220
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5161 AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA 5220
Qy      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5221 AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA 5280
Qy      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5281 ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT 5340
Qy      5341 TAAATCTGAATAAAGAATTCTTCCTGTTCACCTGGCTCTTTTCTTCTCCATGCACCTGAGCA 5400
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5341 TAAATCTGAATAAAGAATTCTTCCTGTTCACCTGGCTCTTTTCTTCTCCATGCACCTGAGCA 5400
Qy      5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC 5460
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5401 TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAAC 5460
Qy      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5461 CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5521 CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        ||||||||||||||||||||||||||||||||||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 8

AR721150

LOCUS AR721150 5674 bp DNA linear PAT 07-OCT-2005

DEFINITION Sequence 8 from patent US 6946289.

ACCESSION AR721150

VERSION AR721150.1 GI:77372626

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 5674)

AUTHORS Guagler,B., van den Eynde,B., van der Bruggen,P. and
Boon-Falleur,T.

TITLE Isolated nucleic acid molecules coding for tumor rejection antigen
precursor Mage-6 and uses thereof

JOURNAL Patent: US 6946289-A 8 20-SEP-2005;

Ludwig Institute for Cancer Research; New York, NY

FEATURES Location/Qualifiers

source 1. .5674

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 5674; DB 2; Length 5674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCACCCCTG 120
        |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
        |||
Db    121 CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
        |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
        |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
        |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
        |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
        |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
        |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600
        |||
Db    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA 600

Qy    601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT 660
        |||
Db    601 CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT 660

Qy    661 CACCCCCACCCACCCACGCCCCTCCACCCCAAGGCAGGATCCGGTTCCTCG 720
        |||
Db    661 CACCCCCACCCACCCACGCCCCTCCACCCCAAGGCAGGATCCGGTTCCTCG 720

Qy    721 CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780
        |||
Db    721 CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA 780

Qy    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840
        |||
Db    781 GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG 840
```

Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTATTTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCCGCATTAGGGTCAGG	1800

Db	1741	 GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCCGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	 ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	 CCACTCACATTCCCATACCTACCCCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	 TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	 GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	 TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	 ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	 GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	 GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	 GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	 TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	 AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTAACCA	2520
Db	2461	 TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTAACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	 CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	 ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAGGGGTGAGCCCTGGACACC	2700

Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACC	AAAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT		2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT		2760
Qy	2761	CATTCTCAGAGGGTGA	CTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGA	CTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG		2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG		2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG		2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG		2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG		3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG		3000
Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC		3060
Db	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC		3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT		3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT		3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT		3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT		3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG		3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG		3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA		3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA		3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG		3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG		3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT		3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT		3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC		3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC		3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA		3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA		3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG		3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG		3600

Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAATTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAATTCTC	3780
Qy	3781	AGCTGAGGCCCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Db	3781	AGCTGAGGCCCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840
Qy	3841	CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500

Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAA	5220
Qy	5221	AGAATAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAATAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460

```

Db      5401  TCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Qy      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Db      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Db      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
Db      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
Qy      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
Db      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 9

AC152005/c

LOCUS AC152005 88597 bp DNA linear PRI 20-OCT-2004

DEFINITION Homo sapiens chromosome X clone CTC-233o10 map q28, complete sequence.

ACCESSION AC152005

VERSION AC152005.1 GI:54306089

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 88597)

AUTHORS Mallon,A.M., Platzner,M., Bate,R., Gloeckner,G., Botcherby,M.R., Nordsiek,G., Strivens,M.A., Kioschis,P., Dangel,A., Cunningham,D., Straw,R.N., Weston,P., Gilbert,M., Fernando,S., Goodall,K., Hunter,G., Greystrom,J.S., Clarke,D., Kimberley,C., Goerdes,M., Blechschmidt,K., Rump,A., Hinzmann,B., Mundy,C.R., Miller,W., Poustka,A., Herman,G.E., Rhodes,M., Denny,P., Rosenthal,A. and Brown,S.D.

TITLE Comparative genome sequence analysis of the Bpa/Str region in mouse and Man

JOURNAL Genome Res. 10 (6), 758-775 (2000)

PUBMED 10854409

REFERENCE 2 (bases 1 to 88597)

AUTHORS Lagemann,D. and Platzner,M.

TITLE Direct Submission

JOURNAL Submitted (20-OCT-2004) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

COMMENT ----- Genome Center

Center: Institute of Molecular Biotechnology

Center code: IMB

Web site: <http://genome.imb-jena.de/>

Contact: gscj-submit@genome.imb-jena.de

----- Project Information

Center project name: 233o

Center clone name: CTC-233o10

----- Summary Statistics

Sequencing vector: M13mpl8; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329
Consensus quality: 88596 bases at least Q40
Consensus quality: 88597 bases at least Q30
Consensus quality: 88597 bases at least Q20
Quality coverage: 21.98x

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Neighboring sequence information:
This clone is overlapped by RP11-76K17, G248-85942H2, G248-86799C8, Qc-15B1, Qc-3H10, Qc-13B12.

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

FEATURES Location/Qualifiers
 source 1. .88597
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="X"
 /map="q28"
 /clone="CTC-233o10"
 source 1. .8123
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="G248-85942H2"
 /note="overlapping clone"
 source 1. .14265
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="G248-86799C8"
 /note="overlapping clone"
 source 1. .35153
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="RP11-76K17"
 /note="overlapping clone"
 source 49506. .88597
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Qc-15B1"
 /note="overlapping clone"
 source 63059. .88597

```

/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Qc-3H10"
/note="overlapping clone"
source      84876. .88597
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Qc-13B12"
/note="overlapping clone"
misc_feature 3461. .3739
/note="pcr product sequence only"
misc_feature 46152. .46248
/note="single stranded/single chemistry region"

ORIGIN

Query Match          98.1%;   Score 5567.8;   DB 5;   Length 88597;
Best Local Similarity 99.6%;   Pred. No. 0;
Matches 5655;   Conservative    0;   Mismatches    17;   Indels      7;   Gaps      7;

Qy      1  CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC  60
      |||
Db      58574 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC  58515

Qy      61  ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG  120
      |||
Db      58514 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG  58455

Qy      121  CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG  180
      |||
Db      58454 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG  58395

Qy      181  TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG  240
      |||
Db      58394 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG  58335

Qy      241  CCCA-GCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCC  299
      |||
Db      58334 CCCAGGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCC  58275

Qy      300  CAGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTT  359
      |||
Db      58274 CAGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTT  58215

Qy      360  CTCAGGCTGGGCCACCCCGACCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGA  419
      |||
Db      58214 CTCAGGCTGGGCCACCCCGACCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAG  58155

Qy      420  GCTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACA  479
      |||
Db      58154 AGCTCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACA  58095

Qy      480  TCATGCTCAGGATTC TAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAA  539
      |||
Db      58094 TCATGCTCAGGATTC TAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAA  58035

Qy      540  CCCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCC  599
      |||
Db      58034 CCCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCC  57975

```

Qy	600	ACCCACATCCCCACCCATCCCTCAACCCTGATGCCCATCCGCCCAGCCATTCCACCC	659
Db	57974	ACCCACATCCCCACCCATCCCTCAACCCTGATGCCCATCCGCCCAGCCATTCCACCC	57915
Qy	660	TCACCCCCACCCCCACCCCCACGCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCC	719
Db	57914	TCACCCCCACCCCCACCCCCACGCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCC	57855
Qy	720	GCCAGGAAACATCCGGGTGCCCCGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAG	779
Db	57854	GCCAGGAAACATCCGGGTGCCCCGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAG	57795
Qy	780	AGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAG	839
Db	57794	AGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAG	57735
Qy	840	GCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAAT	899
Db	57734	GCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAAT	57675
Qy	900	AGAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAG	959
Db	57674	AGAGAGCCCCAAATATTCCAGCGCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAG	57615
Qy	960	ACGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTT	1019
Db	57614	ACGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTT	57555
Qy	1020	CTTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAG	1079
Db	57554	CTTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAG	57495
Qy	1080	GGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCC	1139
Db	57494	GGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCC	57435
Qy	1140	CCCAAGACTGCACTCCAATCCCCACTCCACCCCATTCGCATTCCCATTCCCCACCCAAC	1199
Db	57434	CCCAAGACTGCACTCCAATCCCCACTCCACCCCATTCGCATTCCCATTCCCCACCCAAC	57375
Qy	1200	CCCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCAC	1259
Db	57374	CCCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCAC	57315
Qy	1260	CACCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAA	1319
Db	57314	CACCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAA	57255
Qy	1320	CCCCACCCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTGGCAGAATC	1379
Db	57254	CCCCACCCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTGGCAGAATC	57195
Qy	1380	CGGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGAC	1439
Db	57194	CGGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGATGGCCCGATGTGAAACCACTGAC	57135
Qy	1440	TTGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTTAATGGTTCTGAGGGGCGGCTTGA	1499
Db	57134	TTGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTTAATGGTTCTGAGGGGCGGCTTGA	57075
Qy	1500	GATCCACTGAGGGGAGTGGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAG	1559

Db	57074	 GATCCACTGAGGGGAGTGGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAG	57015
Qy	1560	GACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCT	1619
Db	57014	 GACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCT	56955
Qy	1620	GCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTC	1679
Db	56954	 GCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTC	56895
Qy	1680	CCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGT	1739
Db	56894	 CCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGT	56835
Qy	1740	TGGTCAGGAGA-GGCAGGGCCCAGGCATCAAGGTCCA-GCATCCGCCCGGCATTAGGGTC	1797
Db	56834	 TGGTCAGGAGAGGGCAGGGCCCAGGCATCAAGGTCCAGGCATCCGCCCGGCATTAGGGTC	56775
Qy	1798	AGGACCCTGGGAGGGAAGTGGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCC	1857
Db	56774	 AGGACCCTGGGAGGGAAGTGGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCC	56715
Qy	1858	ACCCCACTCACATTCCCATACTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTG	1917
Db	56714	 ACCCCACTCACATTCCCATACTACCCCTACCCCCAACCTCATCTTGTCAGAATCCCTG	56655
Qy	1918	CTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCAT	1977
Db	56654	 CTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCAT	56595
Qy	1978	CCAGGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCC	2037
Db	56594	 CCAGGG-CTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCC	56536
Qy	2038	TACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCT	2097
Db	56535	 TACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCT	56476
Qy	2098	GAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATT-GCAT	2156
Db	56475	 GAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTAGCAT	56416
Qy	2157	GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGA	2216
Db	56415	 GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGA	56356
Qy	2217	CCTTGGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACA	2276
Db	56355	 CCTTGGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACA	56296
Qy	2277	TATGGCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGG	2336
Db	56295	 TATGGCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGG	56236
Qy	2337	GGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTT	2396
Db	56235	 GGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTT	56176
Qy	2397	CATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCC	2456

Db	56175	CATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCC	56116
Qy	2457	CCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGT	2516
Db	56115	CCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGT	56056
Qy	2517	ACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGAT	2576
Db	56055	ACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGAT	55996
Qy	2577	GTC TACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGAT	2636
Db	55995	GTC TACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGAT	55936
Qy	2637	GAGTGAGACAGACAAGGCTATTGGAATCCACACCCCAGAACC AAAGGGGTCAGCCCTGGA	2696
Db	55935	GAGTGAGACAGACAAGGCTATTGGAATCCTCACCACAGAACC AAAGGGGTCAGCCCTGGA	55876
Qy	2697	CACCTCACCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGG	2756
Db	55875	CACCTCACCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGG	55817
Qy	2757	ACCTCATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAG	2816
Db	55816	ACCTCATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAG	55757
Qy	2817	AGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACC	2876
Db	55756	AGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACC	55697
Qy	2877	CCAGGACCAGAACACTGAGGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCCC	2936
Db	55696	CCAGGACCAGAACACTGAGGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTACCCCC	55637
Qy	2937	AGAGAGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTC	2996
Db	55636	AGAGAGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTC	55577
Qy	2997	AGGGACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCA	3056
Db	55576	AGGGACGGGGAGGCC TTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCA	55517
Qy	3057	GGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTC	3116
Db	55516	GGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTC	55457
Qy	3117	CAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGAT	3176
Db	55456	CAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGAT	55397
Qy	3177	GTTTGTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATTGATTTC	3236
Db	55396	GTTTGTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAAC TCTTGATTGATTTC	55337
Qy	3237	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	3296
Db	55336	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	55277
Qy	3297	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCT	3356
Db	55276	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCT	55217

Qy	3357	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT	3416
Db	55216	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT	55157
Qy	3417	TCCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	3476
Db	55156	TCCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	55097
Qy	3477	GGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACA	3536
Db	55096	GGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACA	55037
Qy	3537	CCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCT	3596
Db	55036	CCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCT	54977
Qy	3597	ACTGTCAGTCCGTGTAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACT	3656
Db	54976	ACTGTCAGTCCGTGTAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACT	54917
Qy	3657	TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC	3716
Db	54916	TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC	54857
Qy	3717	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGT	3776
Db	54856	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGT	54797
Qy	3777	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC	3836
Db	54796	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC	54737
Qy	3837	AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	54736	AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	54677
Qy	3897	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Db	54676	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	54617
Qy	3957	TGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTCCTGGGCACCCTGGAGGAGG	4016
Db	54616	TGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTCCTGGGCACCCTGGAGGAGG	54557
Qy	4017	TGCCCACCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCA	4076
Db	54556	TGCCCACCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCA	54497
Qy	4077	CTACCATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGG	4136
Db	54496	CTACCATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGG	54437
Qy	4137	AGGGGCCAAGCACCTCTTGATCCTGGAGTCTTGTTCGAGCAGTAATCACTAAGAAGG	4196
Db	54436	AGGGGCCAAGCACCTCTTGATCCTGGAGTCTTGTTCGAGCAGTAATCACTAAGAAGG	54377
Qy	4197	TGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG	4256
Db	54376	TGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG	54317

Qy	4257	CAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCA	4316
Db	54316	CAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCA	54257
Qy	4317	AAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCG	4376
Db	54256	AAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCG	54197
Qy	4377	GCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATA	4436
Db	54196	GCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATA	54137
Qy	4437	ATCAGATCATGCCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGG	4496
Db	54136	ATCAGATCATGCCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGG	54077
Qy	4497	GCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATG	4556
Db	54076	GCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATG	54017
Qy	4557	GGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTGGTGCAGG	4616
Db	54016	GGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTGGTGCAGG	53957
Qy	4617	AAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGT	4675
Db	53956	AAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGT	53897
Qy	4676	GGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGG	4735
Db	53896	GGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGG	53837
Qy	4736	TCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGG	4795
Db	53836	TCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGG	53777
Qy	4796	AAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGC	4855
Db	53776	AAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGC	53717
Qy	4856	ACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTC	4915
Db	53716	ACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTC	53657
Qy	4916	ACTCTGAAGAGAGCGGTCAGTGTTCCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGG	4975
Db	53656	ACTCTGAAGAGAGCGGTCAGTGTTCCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGG	53597
Qy	4976	AGATTTATCTTTGTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAA	5035
Db	53596	AGATTTATCTTTGTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAA	53537
Qy	5036	TGAACTTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTT	5095
Db	53536	TGAACTTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTT	53477
Qy	5096	AAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG	5155
Db	53476	AAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG	53417
Qy	5156	ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGA	5215

```

|||||
Db      53416 ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGA 53357
Qy      5216 GATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCT 5275
|||||
Db      53356 GATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCT 53297
Qy      5276 GTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGA 5335
|||||
Db      53296 GTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGA 53237
Qy      5336 GAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACT 5395
|||||
Db      53236 GAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACT 53177
Qy      5396 GAGCATCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACT 5455
|||||
Db      53176 GAGCATCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACT 53117
Qy      5456 CATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAG 5515
|||||
Db      53116 CATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAG 53057
Qy      5516 ATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGA 5575
|||||
Db      53056 ATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGA 52997
Qy      5576 GAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTC 5635
|||||
Db      52996 GAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTC 52937
Qy      5636 CTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
|||||
Db      52936 CTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 52898

```

RESULT 10

AC153070/c

LOCUS AC153070 40359 bp DNA linear PRI 01-DEC-2004

DEFINITION Homo sapiens chromosome X clone Qc-15B1 map q28, complete sequence.

ACCESSION AC153070

VERSION AC153070.1 GI:56158998

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 40359)

AUTHORS Platzter,M., Michaelis,E. and Heinze,I.

TITLE Chromosome X genomic sequence

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 40359)

AUTHORS Lagemann,D. and Platzter,M.

TITLE Direct Submission

JOURNAL Submitted (01-DEC-2004) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

COMMENT ----- Genome Center

Center: Institute of Molecular Biotechnology

Center code: IMB

Web site: <http://genome.imb-jena.de/>

Contact: gscj-submit@genome.imb-jena.de

----- Project Information

Center project name: X65

Center clone name: Qc-15B1

----- Summary Statistics

Sequencing vector: M13mpl8; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 40359 bases at least Q40

Consensus quality: 40359 bases at least Q30

Consensus quality: 40359 bases at least Q20

Quality coverage: 20.90x

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Neighboring sequence information:

This clone is overlapped by CTC-233o10, Qc-3H10, Qc-13B12.

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than

1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

FEATURES	Location/Qualifiers
source	1. .40359 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="X" /map="q28" /clone="Qc-15B1"
source	1. .39172 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="CTC-233o10" /note="overlapping clone"
source	13557. .40359 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="Qc-3H10" /note="overlapping clone"
source	35451. .40359 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="Qc-13B12" /note="overlapping clone"

ORIGIN

Query Match 97.6%; Score 5535.8; DB 5; Length 40359;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 5642; Conservative 0; Mismatches 27; Indels 10; Gaps 8;

Qy	1	CCCGGGGCACCACTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC	60
Db	9070	CCCGGGGCACCACTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC	9011
Qy	61	ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG	120
Db	9010	ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG	8951
Qy	121	CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Db	8950	CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	8891
Qy	181	TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Db	8890	TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	8831
Qy	241	CCCA-GCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCC	299
Db	8830	CCCAGGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCC	8771
Qy	300	CAGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTT	359
Db	8770	CAGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTT	8711
Qy	360	CTCAGGCTGGGCCACCCCGACCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGA	419
Db	8710	CTCAGGCTGGGCCACCCCGACCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAG	8651
Qy	420	GCTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACA	479
Db	8650	AGCTCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACA	8591
Qy	480	TCATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAA	539
Db	8590	TCATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAA	8531
Qy	540	CCCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCC	599
Db	8530	CCCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCC	8471
Qy	600	ACCCACATCCCCACCCATCCCTCAACCCTGATGCCATCCGCCAGCCATTCCACCC	659
Db	8470	ACCCACATCCCCACCCATCCCTCAACCCTGATGCCATCCGCCAGCCATTCCACCC	8411
Qy	660	TCACCCCAACCCCAACCCACGCCCCTCCACCCCAACCCAGGCAGGATCCGGTTCCC	719
Db	8410	TCACCCCAACCCCAACCCACGCCCCTCCACCCCAACCCAGGCAGGATCCGGTTCCC	8351
Qy	720	GCCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAG	779
Db	8350	GCCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAG	8291
Qy	780	AGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAG	839
Db	8290	AGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAG	8231

Qy	840	GCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAAT	899
Db	8230	GCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAAT	8171
Qy	900	AGAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAG	959
Db	8170	AGAGAGCCCCAAATATTCCAGCGCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAG	8111
Qy	960	ACGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTT	1019
Db	8110	ACGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCACGTT	8051
Qy	1020	CTTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAG	1079
Db	8050	CTTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAG	7991
Qy	1080	GGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCC	1139
Db	7990	GGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCC	7931
Qy	1140	CCCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAAC	1199
Db	7930	CCCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAAC	7871
Qy	1200	CCCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCAC	1259
Db	7870	CCCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCAC	7811
Qy	1260	CACCTTCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAA	1319
Db	7810	CACCTTCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAA	7751
Qy	1320	CCCCACCCTCATCTCTCATGTGCCCCACTCCCATCGCTCCCCCATCTTGGCAGAATC	1379
Db	7750	CCCCACCCTCATCTCTCATGTGCCCCACTCCCATCGCTCCCCCATCTTGGCAGAATC	7691
Qy	1380	CGGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGAC	1439
Db	7690	CGGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGATGGCCCGATGTGAAACCACTGAC	7631
Qy	1440	TTGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGA	1499
Db	7630	TTGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGA	7571
Qy	1500	GATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAG	1559
Db	7570	GATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAG	7511
Qy	1560	GACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCT	1619
Db	7510	GACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCT	7451
Qy	1620	GCCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTC	1679
Db	7450	GCCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTC	7391
Qy	1680	CCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGT	1739
Db	7390	CCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGT	7331
Qy	1740	TGGTCAGGAGA-GGCAGGGCCAGGCATCAAGGTCCA-GCATCCGCCCGGCATTAGGGTC	1797

Db	7330	 TGGTCAGGAGAGGGCAGGGCCCAGGCATCAAGGTCCAGGCATCCGCCCGGCATTAGGGTC	7271
Qy	1798	AGGACCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCC	1857
Db	7270	 AGGACCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCC	7211
Qy	1858	ACCCCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTCTCAGAATCCCTG	1917
Db	7210	 ACCCCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTCTCAGAATCCCTG	7151
Qy	1918	CTGTCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCAT	1977
Db	7150	 CTGTCAACCCACGGAAGCCACGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCAT	7091
Qy	1978	CCAGGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCC	2037
Db	7090	 CCAGGG-CTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCC	7032
Qy	2038	TACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCT	2097
Db	7031	 TACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCT	6972
Qy	2098	GAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATT-GCAT	2156
Db	6971	 GAGACTGAGGCTGCCACTTTTGGCCTCAAGAATCAGAATGATGGGGACTCAGATTAGCAT	6912
Qy	2157	GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGA	2216
Db	6911	 AGGGGTGGGACCCAGGCCTGCAAGGCTTACGAGGAGGAAGAGGAGGGAGGACTCAGGGGA	6852
Qy	2217	CCTTGGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACA	2276
Db	6851	 CCTTGGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACA	6792
Qy	2277	TATGGCCCATATTTCTTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGG	2336
Db	6791	 TATGGCCCATATTTCTTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGG	6732
Qy	2337	GGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTT	2396
Db	6731	 GGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTT	6672
Qy	2397	CATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCC	2456
Db	6671	 CATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCC	6612
Qy	2457	CCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGT	2516
Db	6611	 CCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGT	6552
Qy	2517	ACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGAT	2576
Db	6551	 ACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAA---GGGAT	6495
Qy	2577	GTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGAT	2636
Db	6494	 GTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGAT	6435
Qy	2637	GAGTGAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGGTCAGCCCTGGA	2696

Db	6434	GAGTGAGACAGACAAGGCTATTGGAATCCTCACCCCAGAACCAAAGGGGCCAGCCCTGGA	6375
Qy	2697	CACCTCACCCAGGATGTGGCTTCTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGG	2756
Db	6374	CACCTCACCCAGGATGTGGCTTC-TTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGG	6316
Qy	2757	ACCTCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAG	2816
Db	6315	ACCTCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAG	6256
Qy	2817	AGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACC	2876
Db	6255	AGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACC	6196
Qy	2877	CCAGGACCAGAACACTGAGGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCC	2936
Db	6195	CCAGGACCAGAACACTGAGGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCC	6136
Qy	2937	AGAGAGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTC	2996
Db	6135	AGAGAGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTC	6076
Qy	2997	AGGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCA	3056
Db	6075	AGGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCA	6016
Qy	3057	GGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTC	3116
Db	6015	GGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTC	5956
Qy	3117	CAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGAT	3176
Db	5955	CAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGAT	5896
Qy	3177	GTTTGTCCCCCTCCTGTCCCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTGATTTC	3236
Db	5895	GTTTGTCCCCCTCCTGTCCCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTGATTTC	5836
Qy	3237	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	3296
Db	5835	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	5776
Qy	3297	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCT	3356
Db	5775	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCT	5716
Qy	3357	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGAT	3416
Db	5715	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGAT	5656
Qy	3417	TCCCTTCTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	3476
Db	5655	TCCCTTCTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	5596
Qy	3477	GGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACA	3536
Db	5595	GGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACA	5536
Qy	3537	CCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCT	3596
Db	5535	CCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCT	5476

Qy	3597	ACTGTCAGTCCTGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACT	3656
Db	5475	ACTGTCAGTCCTGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACT	5416
Qy	3657	TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCAC	3716
Db	5415	TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCAC	5356
Qy	3717	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGT	3776
Db	5355	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGT	5296
Qy	3777	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCC	3836
Db	5295	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCC	5236
Qy	3837	AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	5235	AGCTCCTGCCCACACTCCTGCCTGTTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	5176
Qy	3897	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Db	5175	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	5116
Qy	3957	TGTGTGTGCAGGCTGCCACCTCCTCCTCCTCCTCCTGCTGCTGGTCCCTGGGCACCCTGGAGGAGG	4016
Db	5115	TGTGTGTGCAGGCTGCCGCTCCTCCTCCTCCTCCTGCTGCTGGTCCCTGGGCACCCTGGAGGAGG	5056
Qy	4017	TGCCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCA	4076
Db	5055	TGCCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCA	4996
Qy	4077	CTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGG	4136
Db	4995	CTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGG	4936
Qy	4137	AGGGGCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGG	4196
Db	4935	AGGGGCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGG	4876
Qy	4197	TGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG	4256
Db	4875	TGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG	4816
Qy	4257	CAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCA	4316
Db	4815	CAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCA	4756
Qy	4317	AAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCG	4376
Db	4755	AAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCG	4696
Qy	4377	GCCACTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATA	4436
Db	4695	GCCACTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATA	4636
Qy	4437	ATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGG	4496
Db	4635	ATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGG	4576

Qy	4497	GCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATG	4556
Db	4575	GCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATG	4516
Qy	4557	GGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGG	4616
Db	4515	GGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGG	4456
Qy	4617	AAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGT	4675
Db	4455	AAAAGTACCTGGAGTACCGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGT	4396
Qy	4676	GGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGG	4735
Db	4395	GGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGG	4336
Qy	4736	TCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGG	4795
Db	4335	TCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGG	4276
Qy	4796	AAGAGGGAGTC TGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGC	4855
Db	4275	AAGAGGGAGTC TGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGC	4216
Qy	4856	ACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTC	4915
Db	4215	ACCTTCCAGGGCCGCGTGCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTC	4156
Qy	4916	ACTCTGAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGG	4975
Db	4155	ACTCTGAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTGTTGGGTGACTTGG	4096
Qy	4976	AGATTTATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAA	5035
Db	4095	AGATTTATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAA	4036
Qy	5036	TGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTT	5095
Db	4035	TGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTT	3976
Qy	5096	AAGGGTAAGAGTCTTGTGTTTTATT CAGATTGGGAAATCCATTCTATTTTGTGAATTGGG	5155
Db	3975	AAGGGTAAGAGTCTTGTGTTTTATT CAGATTGGGAAATCCATTCTATTTTGTGAATTGGG	3916
Qy	5156	ATAATAACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGA	5215
Db	3915	ATAATAACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGA	3856
Qy	5216	GATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCT	5275
Db	3855	GATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCT	3796
Qy	5276	GTAAAATTTTTAAAGATATATGCATACCTGGATTTCCCTGGCTTCTTTGAGAATGTAAGA	5335
Db	3795	GTAAAATTTTTAAAGATATATGCATACCTGGATTTCCCTGGCTTCTTTGAGAATGTAAGA	3736
Qy	5336	GAAATTAAATCTGAATAAAGAATTCTTCCTGTTTACTGGCTCTTTTCTTCTCCATGCACT	5395
Db	3735	GAAATTAAATCTGAATAAAGAATTCTTCCTGTTTACTGGCTCTTTTCTTCTCCATGCACT	3676
Qy	5396	GAGCATCTGCTTTTTTGAAGGCCCTGGGT TAGTAGTGGAGATGCTAAGGTAAGCCAGACT	5455

```

Db      3675 GAGCATCTGCTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACT 3616
Qy      5456 CATAACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAG 5515
Db      3615 CATAACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAG 3556
Qy      5516 ATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGA 5575
Db      3555 ATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGA 3496
Qy      5576 GAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTC 5635
Db      3495 GAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTC 3436
Qy      5636 CTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
Db      3435 CTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 3397

```

RESULT 11

AC116666/c

LOCUS AC116666 169351 bp DNA linear PRI 06-FEB-2003

DEFINITION Homo sapiens chromosome X clone RP11-329E24 map q28, complete sequence.

ACCESSION AC116666 AC024727 AF134576

VERSION AC116666.2 GI:28261468

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 169351)

AUTHORS Galgoczy, P., Wen, G. and Platzner, M.

TITLE Chromosome X genomic sequence

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 169351)

AUTHORS Platzner, M.

TITLE Direct Submission

JOURNAL Submitted (02-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

REFERENCE 3 (bases 1 to 169351)

AUTHORS Platzner, M.

TITLE Direct Submission

JOURNAL Submitted (06-FEB-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

COMMENT On or before Feb 6, 2003 this sequence version replaced gi:13786263, gi:19881535.

----- Genome Center

Drafting Center: Washington Univ. Genome Sequencing Center

Finishing Center: Institute of Molecular Biotechnology

Center code: IMB

Web site: <http://genome.imb-jena.de/>

Contact: gscj-submit@genome.imb-jena.de

----- Project Information

Center project name: X164

Center clone name: RP11-329E24

----- Summary Statistics

Sequencing vector: M13, pUC18; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329
Consensus quality: 169243 bases at least Q40
Consensus quality: 169295 bases at least Q30
Consensus quality: 169351 bases at least Q20
Quality coverage: 16.11x

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

This clone was finished using overlapping sequence from accession AC009621 drafted by WIBR.

Neighboring sequence information:

This entry is overlapped by RP1-73F14, RP11-1007I13, RP11-157E12 and covers Qc-3H5, ICRFXc104-3G5, Qc-16C3, Qc-4H4 entirely.

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

FEATURES	Location/Qualifiers
source	1. .169351 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="X" /map="q28" /clone="RP11-329E24" /clone_lib="RPCI human BAC library 11"
source	1. .33333 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="RP1-73F14" /clone_lib="RPCI human PAC library 1"
source	1. .66680 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="RP11-1007I13" /clone_lib="RPCI human BAC library 11"
source	20333. .169351 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="AC009621"
source	31813. .69584 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"

```

/clone="Qc-3H5"
/clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
source 37604. .80648
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="ICRFxc104-3G5"
/clone_lib="ICRF human X specific cosmid library"
source 54954. .98328
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Qc-16C3"
/clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
source 81172. .97869
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Qc-4H4"
/clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
source 132018. .169351
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="RP11-157E12"
/clone_lib="RPCI human BAC library 11"
variation 2148
/note="G substituted in clone: RP1-73F14"
/replace="c"
variation 2251
/note="C substituted in clone: RP1-73F14"
/replace="t"
variation 2651
/note="A substituted in clone: RP1-73F14"
/replace="c"
variation 3309
/note="deleted in clone: RP11-329E24"
/replace=""
variation 3677
/note="G substituted in clone: RP1-73F14"
/replace="t"
variation 5359
/note="A substituted in clone: RP1-73F14"
/replace="g"
variation 5484
/note="T substituted in clone: RP1-73F14"
/replace="a"
variation 6036
/note="C substituted in clone: RP1-73F14"
/replace="t"
variation 7127
/note="C substituted in clone: RP1-73F14"
/replace="g"
variation 7665
/note="T substituted in clone: RP1-73F14"
/replace="a"
variation 7978
/note="A substituted in clone: RP1-73F14"
/replace="t"
variation 7986
/note="deleted in clone: RP11-329E24"

```

```

variation      /replace=""
7996
/note="deleted in clone: RP11-329E24"
/replace=""
variation      8223
/note="C substituted in clone: RP1-73F14"
/replace="t"
variation      8333
/note="A substituted in clone: RP11-329E24 , A substituted
in clone: RP11-1007I13"
/replace="c"
variation      8598
/note="C substituted in clone: RP11-1007I13 , C
substituted in clone: RP11-329E24"
/replace="a"
variation      8737
/note="A substituted in clone: RP1-73F14"
/replace="g"
variation      8879
/note="C substituted in clone: RP1-73F14"
/replace="t"
variation      8932
/note="G substituted in clone: RP1-73F14"
/replace="c"
variation      9021
/note="deleted in clone: RP1-73F14"
/replace=""
variation      9351
/note="T substituted in clone: RP1-73F14"
/replace="c"
variation      9356
/note="C substituted in clone: RP1-73F14"
/replace="g"
variation      10146
/note="deleted in clone: RP11-329E24"
/replace=""
variation      10317
/note="G substituted in clone: RP1-73F14"
/replace="a"

```

Query Match 48.7%; Score 2763.2; DB 5; Length 169351;
 Best Local Similarity 74.7%; Pred. No. 0;
 Matches 4348; Conservative 0; Mismatches 1118; Indels 354; Gaps 56;

```

Qy      1 CCCGGGGCACCACCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      || || || || || || || || || || || || || || || || || || || || ||
Db      53899 CCATGAGAACCCCATCCTCCCCAGGCCCCACTACTCTCATCCCACCCACCCACCCCT 53840

Qy      61 ATCCAAACATCTTCACGCTACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      || || || || || || || || || || || || || || || || || || || || ||
Db      53839 CATCTACCCTACCCTACCCCCCTATCCCTACATTCTGGTAGAATCCGGTTTCGCCCTG 53780

Qy      121 CTCTCAACCCAGGGAAG-CCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTG 179
      || || || || || || || || || || || || || || || || || || || || ||
Db      53779 CTTTCAACCGAGGGAATCCCGGGTGCCCGGATGTGACACCACTGACTTG-GCGTTGGGG 53721

Qy      180 GTTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGG 239
      || || || || || || || || || || || || || || || || || || || || ||
Db      53720 GTCAAAGAGAAGCGAAGTTCTCGCTCTGAGTGGCGGCTTGAGATTGGTGGAGGGAAGTGG 53661

Qy      240 GCCCA-GCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACC 298

```

Db	53660	GTCCAGGCTCTGTGAAGAGGCAAGGTGAGACTCTAAGGGAGGACTCAGGAGGCCCCACC	53601
Qy	299	CCAGATAGAGGACCCCAAATAATCC-----CTTCATGCCAGTCTCTGGACCATCTGG	349
Db	53600	CCAGATAGAGGGCCCCAAATAATCCAGCACTACTCTGCTGCCAGCCCTAAACCACCTGG	53541
Qy	350	TGGTGGACTTCTCAGGCTGGGGCACCCCCAGCCCCCT-----TGCTGCTTAAACCA	400
Db	53540	GGGCGGACTTCTCAGTCTGGGGCACTCCCTGCACCCTGCCAGCCCCCTGTGGCTTAAGCCG	53481
Qy	401	CTGGGGACTC-GAAGTCAGAGCTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAG	459
Db	53480	CAAGGGACTCTGGAGTCAGAGCTTCGTGTGACCAAGGCAGGGCTGGTTAGGAGAGGGCAG	53421
Qy	460	CGTCCAGGCTCTGCCAGACATCATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAG	519
Db	53420	TGGCCAAGCTCTGCCAGGCATCAACATCAGGACCCTAAGTGAGGGCTGAGGGCCCCAAC	53361
Qy	520	ACCC---CACTCCCCTGACCCAAACCCCACTCCAATGCTCACTCCCCTGACCCAACCCCC	576
Db	53360	CCCCATTCCCATCCCCCACCACCCATCCCATTTCATCCCCATCCCCACCTCCATCCCCCA	53301
Qy	577	TCTTCATTGTTCATTCCAACCCCCACCCACATCCCCACCCATCCCTCAACCCTGATGC	636
Db	53300	CCAGAACCCCTATCCCCCACCAGAAACCTATCCTGCCCACTCCCCACCACGTTCATCCC	53241
Qy	637	CCATCCGCCCA-GCCATTCCACCCTCACCCCCACCCCAACCCCAACCCCACTCCCACCC	695
Db	53240	TACTCCCACCATTCCCATCTTCCCCACCCCTGACCCTCCTCCTCACCCCTCCCACCCCCC	53181
Qy	696	CCACCCAGGCAGGATCCGG-----TTCCCGCCAGGAAACATCCGGGTGCCCCG	742
Db	53180	ACACCCTGGCAGAATTCCGGTTCTGCTCCTGCTTTCAACCCAGGGAATCCCTGGGTGACCA	53121
Qy	743	GATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGAGAAGCGAGGTTTCCATTCTGAG	802
Db	53120	GATGTGGTGCCACTGTCTTGACACATTTGAGGTCGGAGAGAAGCAAGGGCCTCGCTCTCAG	53061
Qy	803	GGACGGCGTAGAGTTGGCCGAAGGAACCTGACCCAGGCTCTGTGAGGAGGCAAGGTGAG	862
Db	53060	GGGCAGC-TGGAGATCAGCTGAGGGCAGCTGGCCCTGGCTCTGTGAGGATGCAAGGTGAG	53002
Qy	863	AGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATAGAGAGCCCCAAATATTCCAG--	920
Db	53001	ATGCTGAGGGAGGACTAAGGAGTATCCACCCCTGGTAGTGACCCCAAATAATCCAGTG	52942
Qy	921	-CCCCGCCCTTGCTGCCAGCCCTGGGCCACCCGCGGGAAGACGTCTCAGCCTGGGCTGCC	979
Db	52941	CCACCTCTCCTGCTGCTAGCTCTGGACCATCCAGGGCAGGACTCCTTAGGCTGGGCCACC	52882
Qy	980	CCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTCTTCTCCCAAGCTCTGGAA	1039
Db	52881	CCCAGTCCCCCACCCTTAAGCCGCAGGGGA-----CTCAGGAG	52843
Qy	1040	TCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAGGGCACAGGCTCTGCC	1099
Db	52842	ACAGAGCTTGGTATGACCAGGGCAGGACTGGTTAGGAGAGGACAGCTCCAGGCTCTGCC	52783
Qy	1100	AGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAAGACTGCACTCCAATC	1159

Db 52782 AGGAAACAACGTCAGGAACCTAAGGGAAAGCTGAGGCTACCCC----- 52740

Qy 1160 CCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACCCCATCTCCTCAGCTACAC 1219
|||

Db 52739 -----CAC 52737

Qy 1220 CTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACCACCTCCAGCCCCAGCACC 1279
| | | | | | | | | | | | | | | | | | | | | |

Db 52736 GCCAAACTCTATTCCCTGTCCCTACCTCCGTCCCCACCTACACCCCATTC-----CC 52682

Qy 1280 AGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCCAACCCACCTCATCTCTCTCA 1339
| | | | | | | | | | | | | | | | | | | | | |

Db 52681 CACCCCATCCCTACCGGCACCTCTATCCACATCCCCCA----- 52643

Qy 1340 TGTGCCCCACTCCCATCGCCTCCCCCATCTTGGCAGAATCCGGTT-TGCCCCTGCTCTCA 1398
| | | | | | | | | | | | | | | | | | | | | |

Db 52642 -----CCCCTATCTGGCAGAATCCGATTCTGCCCTGATTTC 52604

Qy 1399 ACCCAGGGAAGCCCTGGTAGGCCCCGATGTGAAACCACTGACTTGAACCTCACAGATCTGA 1458
| | | | | | | | | | | | | | | | | | | | | |

Db 52603 ACCCAGGGAAGCCCTAGGGGGCCGGATGTGATGCTGCTGACTTGTGCATTGCGGGTCAGA 52544

Qy 1459 GAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGG 1518
| | | | | | | | | | | | | | | | | | | | | |

Db 52543 GAGAATCAAGG-----GCATGGTTCTGAGAAGCCGACTGAGATCAGCAGAGGGGAATGG 52490

Qy 1519 TTTTAGGCTCTGTGAGGAGGCAAGGTGAGA-TGCTGAGGGAGGACTGAGGAGGCACACAC 1577
| | | | | | | | | | | | | | | | | | | | | |

Db 52489 GCCCGGGCTCTGTGAGGAGGCAAGGTGAGACCCCCGAGGAAGGAATGAGGAAGCCCTCAC 52430

Qy 1578 CCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCC 1637
| | | | | | | | | | | | | | | | | | | | | |

Db 52429 CCA--GATAGAGAACCCCAAATAATCCAGTACTACCTTTGCTGCCAGCCCTGGACCAC-- 52374

Qy 1638 GGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCCCCTGCCACTTAAACCCA 1697
| | | | | | | | | | | | | | | | | | | | | |

Db 52373 --CCAGGGCAGACTTCTCAGGCTGGACCTTCCC--CCCTCCCCACTGCCACTTAAAGCCA 52319

Qy 1698 CAGGGCAATCTGTAGTCATAGCTT-ATGTGACCGGGGCAGGGTTGGTCAGGAGAGGCAGG 1756
| | | | | | | | | | | | | | | | | | | | | |

Db 52318 CAAGGGACTCTGGAGTCAGACCTTGGTGTGACCAGGGAAGGGCCGGTCAGGAGAGG---- 52263

Qy 1757 GCCCAGGCATCAAGGTCCAGCATCCGCCCAGCATTAGGGTCAGGACCTGGGAGGGAACT 1816
| | | | | | | | | | | | | | | | | | | | | |

Db 52262 -----GCAGGGGCCAGGCTCTGTGAGGCATCAAAATCAGGACCCTGAGAGAGAATT 52212

Qy 1817 GAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACCCCACTCACATTCCCAT 1876
| | | | | | | | | | | | | | | | | | | | | |

Db 52211 GAGGGCCCCACCCCAACCCCTATACCCATCCCTAACCCCATACCCACTCTACTTGCATT 52152

Qy 1877 ACCTACCCCTACC-----CCCAACCTCATCTTGTGAGAA-----TCCCTGCTGTC 1922
| | | | | | | | | | | | | | | | | | | | | |

Db 52151 CCCAGCCCCATCCCCACACCTACCCCATCTTGGCAGAATCTGTTTCTTTCCCTGCAGTC 52092

Qy 1923 AACCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCAGG 1982
| | | | | | | | | | | | | | | | | | | | | |

Db 52091 AACCACAGAAGCCCCAGGAATGACAGACAGGCACACCCATTCTGACGTCCACATCCAGG 52032

Qy 1983 GTCTGATGGAGGGAAGGGGCT-----TGAACAGGGCCTCAGGGGAGCAGAGGGAGG-- 2033
| | | | | | | | | | | | | | | | | | | | | |

Db 52031 GCTGAAGGAGGGAAGGGCTTAGTATCATGAGCAGGGCCTCAGGGGAGTCTCTGCTCCTC 51972

Qy	2034	--GCCCTACTGCGAGATGAGGGAGGCCCTCAGAGGACCCAGACCCCTAGGA-----C	2082
Db	51971	AAGCCCTGCTGGGAGTAAAGGGAGGCCTCAGGGAACCCAGGTCCCTCAGGATAGGGGGTCC	51912
Qy	2083	ACCGCACCCCTGTCTGAGACTTGAG--GCTGCCACTTCTTGGCCTCAAGAATCAGAACGATG	2140
Db	51911	ACTCCAACCCTGTCTGAGACTGAGGCGCCTCCTCTTTTCATCCTCGGGAATCAGAGGGATG	51852
Qy	2141	GGGACTCAGATTGCATGGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGA	2200
Db	51851	GAGACTCACGTCAGCAGAGGGTGGGGCCCAACCCTGCCAGGATCAAGGAGAGGAAGAAGA	51792
Qy	2201	GGGAGGACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCA	2260
Db	51791	GGGAGGACTCAGGGTACCTTTGAGTCCAGAACAATGGGGACCTTGTCCCTGGGAGGTCCA	51732
Qy	2261	GGGCACGGTGGCCACATATGGCCCATATTTCTGTCATCTTTGAGGTGAC----AGGACAG	2316
Db	51731	GTGCACAGTGGCCACCTGTAGCCCATGCTTGCTGCACCTTCTGGGTGACAAAGAGGAGAG	51672
Qy	2317	AGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATAT	2376
Db	51671	GGCTGTGGTCAGAGCAGTGGTGACTCAGGTGAGCAGAGGGAGGAGTCCAGCATCTGCAG	51612
Qy	2377	GGCCCAAGATGTGCCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGAC	2436
Db	51611	GCCCCAATGTGTGCCCCATTCATGAAGATTGGGGATA-CCTTGGCTCAGAAAGAAGGGAC	51553
Qy	2437	TCCACACAGTCTGGCTGTCCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGG	2496
Db	51552	CCCACAGAGTCTGGCTGTCCCCTGATTTTTGCTCAGAGGGGACCAAATCAAGGATAGCCC	51493
Qy	2497	TATGTTCCATTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGG	2556
Db	51492	TATGTGCCAACCTCATTGTGCCACAGGAAAGAAGTTGAAGAGCCCTCAGGGTGATGGGG	51433
Qy	2557	TCTTGGGGTAAAGGGGGGATGTCTACTCATGTGAGGAATTGGGGGTTGAGGAAGCACAG	2616
Db	51432	TCTTGCAGTAAAGGGGAGCTATCTGCTCATCTCAGGGGGTTTCAGGTTGAGGAATGGCAG	51373
Qy	2617	GCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCAGAA	2676
Db	51372	GCCCCATCACG----ATGAAGAGTAACCCACAGGAGGCCATAGAAACACTCACCCAGAA	51317
Qy	2677	CCAAAGGGGTCAGCCCTGGACACCTCA-----CCCAGGATGTGGCTTCTTTTTCAC	2727
Db	51316	CCAAAGGGGTCATACCTGGACACCCCATGTGGGGGTGACAGGATGTAGC-TCCATCTCAT	51258
Qy	2728	TCCTGTTTTCCAGATCTGGGGCAGGTGAGGACCTCATTCTCAGAGGGTGACTCAGGTCAAC	2787
Db	51257	TCCTGTTTTCCAGATCTCGGGGAGGTGAGGAACCTGTTCTCCAGGATGACTCAGGTCAAC	51198
Qy	2788	GTAGGGACCCCATCTGGTCTAAAGACAGAGCGGTCCAGGATCTGCCATGCGTTCGGGT	2847
Db	51197	ACAGGGGCCCCCATCTGGTGGATAGACAGAGTGGTCCCAGGATCTGTCTAGTAGTTCCGGT	51138
Qy	2848	GAGGAACATGAGGGAGGACTGAGGGTACCCAGGACCAGAACACTGAGGGAGACTGCACA	2907
Db	51137	GAGGAACATGAGGGACGATTGAGGGCACCCCTTGGGCCAGAACACAGATGAGGACCTCACG	51078

<http://es/ScoreAccessWeb/GetItem.action?AppId=08819669&seqId=609516&ItemName=us...> 8/30/06

Db	50181	AGGCTTCTCACATGCTCCCTCTCTCTCCAGGCCAGTGGGTCTCCATTGCCCAGCTCCTGC	50122
Qy	3846	CCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGC	3905
Db	50121	CCACACTCCTGCCTGTTGCGGTGACCAGAGTCGTCATGTCTCTTGAGCAGAAGAGTCAGC	50062
Qy	3906	ACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGC	3965
Db	50061	ACTGCAAGCCTGAGGAAGGCCCTTGACACCCAAGAAGAGGCCCTGGGCCTGGTGGGTGTGC	50002
Qy	3966	AGGCTGCCAC-----CTCCTCCTCCTCTCCTCTGGTCTCTGGGCA	4004
Db	50001	AGGCTGCCACTACTGAGGAGCAGGAGGCTGTGTCTCCTCCTCTCCTCTGGTCCCAGGCA	49942
Qy	4005	CCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCT	4064
Db	49941	CCCTGGGGGAGGTGCCTGCTGCTGGGTCAACAGGTCTCTCAAGAGTCCTCAGGGAGCCT	49882
Qy	4065	CCGCCTTTCCCACTACCATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCA	4124
Db	49881	CCGCCATCCCCACTGCCATCGATTTCACCTCTATGGAGGCAATCCATTAAGGGCTCCAGCA	49822
Qy	4125	GCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAA	4184
Db	49821	ACCAAGAAGAGGAGGGGCCAAGCACCTCCCCTGACCCAGAGTCTGTGTTCGAGCAGCAC	49762
Qy	4185	TCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGC	4244
Db	49761	TCAGTAAGAAGGTGGCTGACTTGATTCAATTTCTGCTCCTCAAGTATTAAGTCAAGGAGC	49702
Qy	4245	CAGTCACAAAGGCAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCTTG	4304
Db	49701	CGGTACAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTG	49642
Qy	4305	AGATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAG	4364
Db	49641	TGATCTTCGGCAAAGCCTCCGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAG	49582
Qy	4365	CAGACCCCAACCGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCC	4424
Db	49581	CGGACCCCAACAGCAACACCTACACCTTGTACCTGCCTGGG--ACTCCTATGATGGCC	49524
Qy	4425	TGCTGGGTG---ATAATCAGATCATGCCCAAGACAGGCTTCCGATAATTGTCTCTGGTCA	4481
Db	49523	TGGTGGTTGATAATAATCAGATCATGCCCAAGACGGGCCTCCTGATAATCGTCTTGGGCA	49464
Qy	4482	TGATTGCAATGGAGGGCGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGA	4541
Db	49463	TGATTGCAATGGAGGGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGA	49404
Qy	4542	TGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCC	4601
Db	49403	TGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGTGGGGAGCCCAGGAAGCTGCTCACCC	49344
Qy	4602	AAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCAC	4660
Db	49343	AAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCAGCAGTGATCCCATAT	49284
Qy	4661	GCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTG	4720

Db 49283 GCTATGAGTTACTGTGGGGTCCAAGGGCACTCGCTG-----CTTGAAAGTACTGG 49234

Qy 4721 AGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAG 4780
 || | ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 49233 AGCACGTGGTCAGGGTCAATGCAAGAGTTCTCATTTCCTACCCATCCCTGCATGAAGCAG 49174

Qy 4781 CTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG 4840
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 49173 CTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGCTGCAGCCAGGGCCACTGCGAGGG 49114

Qy 4841 GGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCC-TCGTGTGAC 4899
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 49113 GGGCTGGGCCAGTGCACCTTCCAGGGCTCCGTCCACTAGTTCCCCTGCCTTAATGTGAC 49054

Qy 4900 ATGAGGCCCATCTTCTCACTC--TGAAGAGAGCGGTGAGTGTCTCAGTAGTAGGTTTCTG 4957
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 49053 ATGAGGCCCATCTTCTCTCTTTGAAGAGAGCAGTCAACATTCTTAGTAGTGGGTTTCTG 48994

Qy 4958 TTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTT 5017
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 48993 TTCTATTGGATGACTTTGAGATTTGTCTTTGTTTCCTTTTGGGAATTGTTCAAATGTTCC- 48935

Qy 5018 TTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACAC- 5076
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 48934 TTTTAATGGGTGGTTGAATGAACCTCAGCATTCAAATTTATGAATGACAGTAGTCACACA 48875

Qy 5077 -AGTTCGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCC 5135
 ||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 48874 TAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCTTGTTTTTTATTTCAGATTGGGAAATCC 48815

Qy 5136 ATTCTATTTTGTGAATTGGG--ATAATAACAGCAGTGGAAATAAGTACTTA-GAAATGTGA 5192
 |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 48814 ATTCATTTTGTGAATTGGGACATAGTTACAGCAGTGGAAATAAGTATTTCATTTAGAAATG 48755

Qy 5193 AAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCT 5252
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 48754 TGAATGAGCAGTAAAATGATGACA-----TAAAGAAATTAAGATATTTAATTCT 48703

Qy 5253 TGCCTTATACCTCAGTCTATTCTGTAAAA--TTTTTAAAGATATATGCATACCTGGATTT 5310
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 48702 TGCCTTATA-CTCAGTCTACTCGGTAAAATTTTTTTTAAAAATGTGCATACCTGGATTT 48644

Qy 5311 CCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCA 5370
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 48643 CCTTGGCTTCTTTGAGAATGTAAGACAAATTAAATCTGAATAAATCATTCTCCCTGTTCA 48584

Qy 5371 CTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGGGAAGGCCCTGGGTAGTAG 5430
 ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 48583 CTGGCTCATTTATTCTCTATGCACTGAGCATTGCTCTGTGGAAGGCCCTGGGTAAATAG 48524

Qy 5431 TGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCT 5490
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 48523 TGGAGATGCTAAGGTAAGCCAGACTCACCCCTACCCACAGGGTAGTAAAGTCTAGGAGCA 48464

Qy 5491 GCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGG 5550
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 48463 GCAGTCATATAAATTAAGGTGGAGAGGTGCCCTCTAAGATGTAGAGAAAAGTAAGAAAGG 48404

Qy 5551 GGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCAT 5610
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 48403 GGTGAGGGTGTGGGGCTCCAGGTGAGAGTGGTCCAGAGGTAAATGCCCTGTGTGGGGCT 48344

Qy 5611 TTTGGGCTTTGGGAAACTGCAGTTCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGG 5670
 ||||| |||||||||||||||| |||| | ||||||||| ||||| | |||
 Db 48343 TTTGGACTTTGGGAAACTGCAGTTTCTTCGGAGGGAGCTGATTCTAATGAATCGGCGGGG 48284

one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Neighboring sequence information:

This clone is overlapped by RP11-366F6, Qc-7G11, RP1-77B24, ICRFXc104-E0681, Qc-11C8, RP11-329E24, RP11-173J18, Qc-3H5, Qc-3G5, Qc-16C3 and covers Qc-9A9, RP1-73F14 entirely.

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

FEATURES

	Location/Qualifiers
source	1. .173962 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="X" /map="q28" /clone="RP11-1007I13"
source	1. .19170 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="Qc-7G11" /clone_lib="QIZ-derived Xq27.3-Xqter cosmid library" /note="overlapping clone"
source	1. .29165 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="ICRFXC104-E0681" /clone_lib="ICRF human X specific cosmid library no.104" /note="overlapping clone"
source	1. .39874 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="Qc-11C8" /clone_lib="QIZ-derived Xq27.3-Xqter cosmid library" /note="overlapping clone"
source	1. .45885 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="RP11-366F6" /clone_lib="RPCI human BAC 11" /note="overlapping clone"
source	1. .69889 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="RP1-77B24" /clone_lib="RPCI human PAC 1" /note="overlapping clone"

```

source      27601. .63308
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /clone="Qc-9A9"
             /clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
source      55599. .140615
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /clone="RP1-73F14"
             /clone_lib="RPCI human PAC 1"
source      107283. .173962
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /clone="RP11-329E24"
             /clone_lib="RPCI human BAC 11"
             /note="overlapping clone"
source      127615. .173962
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /clone="RP11-173J18"
             /clone_lib="RPCI human BAC 11"
             /note="overlapping clone"
source      139095. .173962
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /clone="Qc-3H5"
             /clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
             /note="overlapping clone"
source      144886. .173962
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /clone="Qc-3G5"
             /clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
             /note="overlapping clone"
source      162236. .162656
             /organism="Homo sapiens"
             /mol_type="genomic DNA"
             /db_xref="taxon:9606"
             /clone="Qc-16C3"
             /clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
             /note="overlapping clone, partially deleted"
variation    278
             /note="C substituted in clone: RP11-366F6"
             /replace="t"
variation    1602
             /note="T substituted in clone: RP11-366F6 , T substituted
             in clone: RP11-1007I13"
             /replace="g"
variation    1971
             /note="C substituted in clone: RP11-1007I13 , C
             substituted in clone: RP11-366F6"
             /replace="t"
variation    2000
             /note="C substituted in clone: ICRFXc104-E0681"
             /replace="t"

```


Qy	460	CGTCCAGGCTCTGCCAGACATCATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAG	519
Db	160702	TGGCCAAGCTCTGCCAGGCATCAACATCAGGACCCTAAGTGAGGGCTGAGGGCCCCCAAC	160643
Qy	520	ACCC---CACTCCCGTGACCCAACCCCCACTCCAATGCTCACTCCCGTGACCCAACCCCC	576
Db	160642	CCCCATTCCCATCCCCCACCACATCCCATTTCATCCCCATCCCCACCTCCATCCCCCA	160583
Qy	577	TCTTCATTGTCATTCCAACCCCCACCCACATCCCCACCCCATCCCTCAACCCTGATGC	636
Db	160582	CCAGAACCCTATCCCCCACCAGAAACCCTATCCTGCCCCACTCCCCACCACGTTTCATCCC	160523
Qy	637	CCATCCGCCCA-GCCATTCCACCCTCACCCCCACCCCCACCCCCACGCCACTCCACCC	695
Db	160522	TACTCCACCATTTCCCATCTTCCCCACCCCTGACCCTCCTCCTCACCTCCCACCCCCC	160463
Qy	696	CCACCCAGGCAGGATCCGG-----TTCCCGCCAGGAAACATCCGGGTGCCCCG	742
Db	160462	ACACCCTGGCAGAATTTCGGTTCTGCTCCTGCTTCAACCCAGGGAATCCCTGGGTGACCA	160403
Qy	743	GATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGAGAAGCGAGTTTCCATTCTGAG	802
Db	160402	GATGTGGTGCCACTGTCTTGACATTTGAGGTCGGAGAGAAGCAAGGGCTCGCTCTCAG	160343
Qy	803	GGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCAGGCTCTGTGAGGAGGCAAGGTGAG	862
Db	160342	GGGCAGC-TGGAGATCAGCTGAGGGCAGCTGGCCCTGGCTCTGTGAGGATGCAAGGTGAG	160284
Qy	863	AGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATAGAGAGCCCCAAATATTCAG--	920
Db	160283	ATGCTGAGGGAGGACTAAGGAGTATCCACCCCTGGTAGTGAGCCCCAAATAATCCAGTG	160224
Qy	921	-CCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGACGTCTCAGCTGGGCTGCC	979
Db	160223	CCACCTCTCCTGCTGCTAGCTCTGGACCATCCAGGGCAGGACTCCTTAGGCTGGGCCACC	160164
Qy	980	CCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTCTTCTCCCCAAGCTCTGGAA	1039
Db	160163	CCCAGTCCCCACCGCTTAAGCCGCAGGGGA-----CTCAGGAG	160125
Qy	1040	TCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAGGGCACAGGCTCTGCC	1099
Db	160124	ACAGAGCTTGGTATGACCAGGGCAGGACTGGTTAGGAGAGGACAGCTCCAGGCTCTGCC	160065
Qy	1100	AGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAAGACTGCACTCCAATC	1159
Db	160064	AGGAAACAACGTCAGGAACCTAAGGGAAAGCTGAGGCTACCCC-----	160022
Qy	1160	CCCACTCCCAACCCATTGCGATTCCCATTCACCCACCCAACCCCCATCTCCTCAGCTACAC	1219
Db	160021	-----CAC	160019
Qy	1220	CTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACCACCCTCCAGCCCCAGCACC	1279
Db	160018	GCCAAACTCTATTCTGTCCCTACCTCCGTCCCCACCTACACCCCCCATTC-----CC	159964
Qy	1280	AGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAACCCACCCCTCATCTCTCTCA	1339
Db	159963	CACCCCATCCCTACCGGCACCTCTATCCACATCCCCCA-----	159925

Qy 1340 TGTGCCCCACTCCCATCGCCTCCCCCATTCTGGCAGAATCCGGTT-TGCCCCCTGCTCTCA 1398
 Db 159924 -----CCCCATCCTGGCAGAATCCGATTCTGCCCCCTGATTTC 159886
 Qy 1399 ACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACCTGACTTGAACCTCACAGATCTGA 1458
 Db 159885 ACCCAGGGAAGCCCTAGGGGGCCGGATGTGATGCTGCTGACTTGTGCATTGCGGGTCAGA 159826
 Qy 1459 GAGAAGCCAGGTTTCATTTAATGGTTCTGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGG 1518
 Db 159825 GAGAATCAAGG-----GCATGGTTCTGAGAAGCCGACTGAGATCAGCAGAGGGGAATGG 159772
 Qy 1519 TTTTAGGCTCTGTGAGGAGGCAAGGTGAGA-TGCTGAGGGAGGACTGAGGAGGCACACAC 1577
 Db 159771 GCGCGGGCTCTGTGAGGAGGCAAGGTGAGACCCCCGAGGAAGGAATGAGGAAGCCCTCAC 159712
 Qy 1578 CCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCC 1637
 Db 159711 CCA--GATAGAGAACCCCCAAATAATCCAGTACTACCTTTGCTGCCAGCCCTGGACCAC-- 159656
 Qy 1638 GGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCCCACTGCCACTTAACCCA 1697
 Db 159655 --CCAGGGCAGACTTCTCAGGCTGGACCTTCCC---CCCTCCCCACTGCCACTTAAGCCA 159601
 Qy 1698 CAGGGCAATCTGTAGTCATAGCTT-ATGTGACCGGGCAGGGTTGGTCAGGAGAGGCAGG 1756
 Db 159600 CAAGGGACTCTGGAGTCAGACCTTGGTGTGACCAGGGAAGGGCCGGTCAGGAGAGG---- 159545
 Qy 1757 GCCCAGGCATCAAGGTCCAGCATCCGCCCCGGCATTAGGGTCAGGACCCTGGGAGGGAAC 1816
 Db 159544 -----GCAGGGGCCAGGCTCTGTGAGGCATCAAAATCAGGACCCTGAGAGAGAATT 159494
 Qy 1817 GAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACCCCACTCACATTCCCAT 1876
 Db 159493 GAGGGCCCCCACCCCAACCCCTATACCCATCCCTAACCCCATACCCACTCTACTTGCATT 159434
 Qy 1877 ACCTACCCCTTACC-----CCCAACCTCATCTTGTGAGAA-----TCCCTGCTGTC 1922
 Db 159433 CCCAGCCCCATCCCCACACCCCTACCCCATCTTGGCAGAATCTGTTTCTTCCCTGCAGTC 159374
 Qy 1923 AACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCAGG 1982
 Db 159373 AACCCACAGAAGCCCCAGGAATGACAGACAGGCACACCCATTCTGACGTCCACATCCAGG 159314
 Qy 1983 GTCTGATGGAGGGAAGGGGCT-----TGAACAGGGCCTCAGGGGAGCAGAGGGAGG-- 2033
 Db 159313 GCTGAAGGAGGGAAGGGCTTAGTATCATGAGCAGGGCCTCAGGGGAGTCTCTGCTCCTC 159254
 Qy 2034 --GCCCTACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCTAGGA-----C 2082
 Db 159253 AAGCCCTGCTGGGAGTAAAGGGAGGCCTCAGGGAACCCAGGTCTCAGGATAGGGGGTCC 159194
 Qy 2083 ACCGCACCCCTGTCTGAGACTGAG--GCTGCCACTTCTGGCCTCAAGAATCAGAACGATG 2140
 Db 159193 ACTCCAACCCGTCTGAGACTGAGGCGCCTCTCTTTTCATCTCGGGAATCAGAGGGATG 159134
 Qy 2141 GGGACTCAGATTGCATGGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGA 2200
 Db 159133 GAGACTCACGTCAGCAGAGGGTGGGGCCCAACCCCTGCCAGGATCAAGGAGAGGAAGAAGA 159074
 Qy 2201 GGGAGGACTCAGGGGACCTTGGAAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCA 2260

Db	159073	 GGGAGGACTCAGGGTACCTTTGAGTCCAGAACAATGGGGACCTTTGCCCTGGGAGGTCCA	159014
Qy	2261	GGGCACGGTGGCCACATATGGCCCATATTTCTGCATCTTTGAGGTGAC----AGGACAG	2316
Db	159013	GTGCACAGTGGCCACCTGTAGCCCATGCTTGCTGCACCTTCTGGGTGACAAAGAGGAGAG	158954
Qy	2317	AGCTGTGGTCTGAGAAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCAGGATCCATAT	2376
Db	158953	GGCTGTGGTCAGAGCAGTGGTGACTCAGGTCAGCAGAGGGAGGAGTCCCAGCATCTGCAG	158894
Qy	2377	GGCCCAAGATGTGCCCCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGAC	2436
Db	158893	GCCCCAATGTGTGCCCCATTTCATGAAGATTGGGGATA-CCTTGGCTCAGAAAGAAGGGAC	158835
Qy	2437	TCCACACAGTCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGG	2496
Db	158834	CCCACAGAGTCTGGCTGTCCCTGATTTTTGCTCAGAGGGGACCAATCAAGGATAGCCC	158775
Qy	2497	TATGTTCCATTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGG	2556
Db	158774	TATGTGCCAACCTCATTTGTGCCACAGGAAGAAGTTGAAGAGCCCTCAGGGTGATGGGG	158715
Qy	2557	TCTTGGGGTAAAGGGGGATGTCTACTCATGTGAGGGAATTGGGGGTTGAGGAAGCACAG	2616
Db	158714	TCTTGCAATAAGGGGAGCTATCTGCTCATCTCAGGGGGTTTCAGGTTGAGGAATGGCAG	158655
Qy	2617	GCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCCAGAA	2676
Db	158654	GCCCCATCACG----ATGAAGAGTAACCCACAGGAGGCCATAGAAACACTCACCCCAGAA	158599
Qy	2677	CCAAAGGGGTCAGCCCTGGACACCTCA-----CCCAGGATGTGGCTTCTTTTTCAC	2727
Db	158598	CCAAAGGGGTCATACCTGGACACCCCATGTGGGGGTGACAGGATGTAGC-TCCATCTCAT	158540
Qy	2728	TCCTGTTTTCAGATCTGGGGCAGGTGAGGACCTCATTCTCAGAGGGTGACTCAGGTCAAC	2787
Db	158539	TCCTGTTTTCAGATCTCGGGGAGGTGAGGAAC TTGTTCTCCGAGGATGACTCAGGTCAAC	158480
Qy	2788	GTAGGGACCCCCATCTGGTCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGGGT	2847
Db	158479	ACAGGGGCCCCATCTGGTGGATAGACAGAGTGGTCCCAGGATCTGTCAGTAGTTCGGGT	158420
Qy	2848	GAGGAACATGAGGGAGGACTGAGGGTACCCAGGACCAGAACACTGAGGGAGACTGCACA	2907
Db	158419	GAGGAACATGAGGGACGATTGAGGGCACCTTGGGCCAGAACACAGATGAGGACCTCACG	158360
Qy	2908	GAAATCAGCCCTGCCCCCTGCTGTCACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGT	2967
Db	158359	GAAATCTGCCCTGCCCCCTGCTGTCACTCCAGAGAGCATGGGCAGGGCTGCTGCTGCAGT	158300
Qy	2968	CCTTCCG--TTATCCTGGGATCATTGATGTGAGGGACGGGGAGGCCTTGGTCTGAGAAGG	3025
Db	158299	CCCCCGACTTACCCTGGGATCATTGGTGTCAGGGATGGGGAGGTCTTTGTC-GAGGGGT	158241
Qy	3026	CTGCGCTCAGGTCACTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCA	3085
Db	158240	CTGCACTCAGGTCACTAGAGGGAGCGTCTTAGGCCCTGCCAGGAGACAAGGTAAGAACGA	158181
Qy	3086	AGCGGGCACCTCACCCAGGACACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCT	3145

Db 158180 AGCAGGTTTCCTACCCAGGACACATGAATTCCAATGCATTTTCAGCATCTCTTCCTGTCTCT 158121

Qy 3146 TCCCCA-AGGACCTAGGCACGTGTGGCCAGATGTTTGTCCCTCCTGTCTCTTCATTCTCT 3204
 |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 158120 TCCCAAGAGGACCTGGGCACGTGTGGCCAGATGTGAGTCTCCTCATGTCTCT---GTTCCC 158064

Qy 3205 TATCATGGATGTGAACTCTTGATTGGATTTCTCAGACCAGCAAAAGGGCAGGATCCAGG 3264
 |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 158063 TATCAGGGATGTGAGCTCTTAATCTGAGTTTCTCAGGCCAGCAAAAGGGTGGGATCCAGG 158004

Qy 3265 CCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGA 3324
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 158003 CCTTGCCAGGAGAAAGGTGAGGGCCCTGTGTGAGCACAGAGGGGACCATTACCCCAAGA 157944

Qy 3325 GAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGCCAGGGCTGT 3384
 | |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 157943 GGGTGGAGACCTCACAGATTCCAGCCTACCCTCCTGTTAGCACTGGGGGCCCTGAGGCTGT 157884

Qy 3385 GCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCAGGAACCAGG 3444
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 157883 GCTTGCACTCTGCACCCTGAGGGCCCATGCATTCTCTTCAGGAGCTCCAGGAAACAGA 157824

Qy 3445 CAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCACAG---- 3500
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 157823 CACTGAGGCCTTGGTCTGAGGCCGTGCCCTCAGGTCACAGAGCAGAGGAGATGCAGACGT 157764

Qy 3501 GGTGTGCCAGCAGTGAATGTTTGCCTGAATGCACACCAAGGGCCCCACCTGCCACAGGA 3560
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 157763 CTAGTGCCAGCAGTGAACGTTTGCCTTGAATGCACACTAATGGCCCCCATCGCCCCAGAA 157704

Qy 3561 CACATAGGACTCCACAGAGTCTGGCCTCA-CCTCCCTACTGTCAGTCCTGTAGAATCGAC 3619
 || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 157703 CATATGGGACTCCAGAGCACCTGGCCTCACCCTCTCTACTGTCAGTCCTGCAGAATCAGC 157644

Qy 3620 CTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCTCCTTCAGGTTTTTCAGGGGA 3679
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 157643 CTCTGCTTGCTTGTGTACCTGAGGTGCCCTCTCACTTTTTCTCCTTCAGGTTCTCAGGGGA 157584

Qy 3680 CAGGCCAACCCAGAGGAC-----AGGATTCCCTGGAGGCCACAGAGGAGCAC 3726
 |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 157583 CAGGCTGACCAGGATCACCAGGAAGCTCCAGAGGATCCCAGGAGGCCCTAGAGGAGCAC 157524

Qy 3727 C-AAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTCAGCTG 3785
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 157523 CAAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCCAAGGTTCACTTTTCTAGCTG 157464

Qy 3786 AGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGC 3845
 |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 157463 AGGCTTCTCACATGCTCCCTCTCTCTCAGGCCAGTGGGTCTCATTGCCCAGCTCCTGC 157404

Qy 3846 CCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGC 3905
 ||||| ||||| |||| | |||| | |||| | |||| | |||| | |||| |

Db 157403 CCACACTCCTGCCTGTTGCGGTGACCAGAGTCGTCTCATGTCTCTTGAGCAGAAGAGTCAGC 157344

Qy 3906 ACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGC 3965
 ||||| ||||| |||| | |||| | |||| | |||| | |||| | |||| |

Db 157343 ACTGCAAGCCTGAGGAAGCCCTTGACACCCAAGAAGAGGCCCTGGGCCTGGTGGGTGTGC 157284

Qy 3966 AGGCTGCCAC-----CTCCTCCTCCTCCTCCTGCTGGTCCCTGGGCA 4004
 ||||| |||| | |||| | |||| | |||| | |||| | |||| |

Db 157283 AGGCTGCCACTACTGAGGAGCAGGAGGCTGTGTCTCTCCTCCTCCTGCTGGTCCCAGGCA 157224

Qy	4005	CCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCT	4064
Db	157223	CCCTGGGGGAGGTGCCTGCTGCTGGGTCAACAGGTCTCTCAAGAGTCCTCAGGGAGCCT	157164
Qy	4065	CCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCA	4124
Db	157163	CCGCCATCCCCACTGCCATCGATTTCCTCTATGGAGGCAATCCATTAAGGGCTCCAGCA	157104
Qy	4125	GCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGGAGCAGTAA	4184
Db	157103	ACCAAGAAGAGGAGGGGCCAAGCACCTCCCCTGACCCAGAGTCTGTGTTCGGAGCAGCAC	157044
Qy	4185	TCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGC	4244
Db	157043	TCAGTAAGAAGGTGGCTGACTTGATTCATTTTCTGCTCCTCAAGTATTAAGTCAAGGAGC	156984
Qy	4245	CAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTG	4304
Db	156983	CGGTCACAAAGGCAGAAATGCTGGAGAGAGTATCAAAAAATTACAAGCGCTGCTTTCCTG	156924
Qy	4305	AGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAG	4364
Db	156923	TGATCTTCGGCAAAGCCTCCGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAG	156864
Qy	4365	CAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCC	4424
Db	156863	CGGACCCACAGCAACACCTACACCCTTGTACCTGCCTGGG--ACTCCTATGATGGCC	156806
Qy	4425	TGCTGGGTG---ATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCCTGGTCA	4481
Db	156805	TGGTGGTTGATAATAATCAGATCATGCCAAGACGGGCTCCTGATAATCGTCTTGGGCA	156746
Qy	4482	TGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGA	4541
Db	156745	TGATTGCAATGGAGGGCAAATGCGTCCCTGAGGAGAAATCTGGGAGGAGCTGAGTGTGA	156686
Qy	4542	TGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCC	4601
Db	156685	TGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGTGGGGAGCCCAGGAAGCTGCTCACCC	156626
Qy	4602	AAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCAC	4660
Db	156625	AAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGCAGGTGCCAGCAGTGATCCCATAT	156566
Qy	4661	GCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTG	4720
Db	156565	GCTATGAGTTACTGTGGGGTCCAAGGGCACTCGCTG-----CTTGAAAGTACTGG	156516
Qy	4721	AGTATGTGATCAAGGTCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAG	4780
Db	156515	AGCACGTGGTCAGGTCATGCAAGAGTTCTCATTTCCTACCCATCCCTGCATGAAGCAG	156456
Qy	4781	CTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG	4840
Db	156455	CTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGCTGCAGCCAGGGCCACTGCGAGGG	156396
Qy	4841	GGACTGGGCCAGTGCACCTTCCAGGGCCGCTCCAGCAGCTTCCCCTGCC-TCGTGTGAC	4899
Db	156395	GGGCTGGGCCAGTGCACCTTCCAGGGCTCCGTCCACTAGTTTCCCCTGCCTTAATGTGAC	156336

Qy	4900	ATGAGGCCCATCTTCTCACTC--TGAAGAGAGCGGTCACTGTTCTCAGTAGTAGGTTTCTG	4957
Db	156335		
Qy	4958	TTCATTGGGTGACTTGGAGATTTATCTTTGTCTCTTTTGGAAATTGTTCAAATGTTTTT	5017
Db	156275		
Qy	5018	TTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACAC-	5076
Db	156216		
Qy	5077	-AGTCTGTGTATATAGTTTAAAGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCC	5135
Db	156156		
Qy	5136	ATTCTATTTTGTGAATTGGG--ATAATAACAGCAGTGAATAAGTACTTA-GAAATGTGA	5192
Db	156096		
Qy	5193	AAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCT	5252
Db	156036		
Qy	5253	TGCCTTATACCTCAGTCTATTCTGTAAAA--TTTTTAAAGATATATGCATACCTGGATTT	5310
Db	155984		
Qy	5311	CCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCA	5370
Db	155925		
Qy	5371	CTGGCTCTTTTCTTCTCCATGCAC TGAGCATCTGCTTTTTTGGGAAGGCCCTGGGT TAGTAG	5430
Db	155865		
Qy	5431	TGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGCTTAGGAGCT	5490
Db	155805		
Qy	5491	GCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAGGGAAAAGTGAGAGAGG	5550
Db	155745		
Qy	5551	GGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCAT	5610
Db	155685		
Qy	5611	TTTGGGCTTTGGGAAACTGCAGTTCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGG	5670
Db	155625		

ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 11495)
 AUTHORS Kipps,T.J. and Wu,Y.
 TITLE Vaccines with enhanced intracellular processing
 JOURNAL Patent: US 6287569-A 9 11-SEP-2001;
 FEATURES Location/Qualifiers
 source 1. .11495
 /organism="unknown"
 /mol_type="unassigned DNA"
 ORIGIN

Query Match 46.8%; Score 2655; DB 2; Length 11495;
 Best Local Similarity 73.6%; Pred. No. 0;
 Matches 4231; Conservative 0; Mismatches 1100; Indels 416; Gaps 50;

Qy	21	CCTCCCCCTACCACCCCCAATCCCTCCCTTTACGCCACCCATCCAAACATCTTCACGCTC	80
Db	5969	CCAGCACCCCTATCCTCCCCAAACCCCACTACCTTATGTCTCATCCCCACCCCAAC	6028
Qy	81	ACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAAGC-C	139
Db	6029	ACCACATATCCCATCCAGGTTGAATCGCATTCGTTTCTGCTTTCACCCAGGGAAGCTC	6088
Qy	140	CAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGGTTAGAGAGAAGCGAGGTTT	199
Db	6089	CAGGTTCTTGGATGTGATGCCAGTGACTTGTGCATTGGGGGTTAGAGAGACGCTAGCTTC	6148
Qy	200	TCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGGCCCA-GCTCTGTAAGGAGG	258
Db	6149	TCAGTCTGACAGGCAGCTTGGGATTGGCAGAGGGAAGCCGGTCCAGGCTCTGTGAGGTGG	6208
Qy	259	CAAGGTGACATGCTGAGGGAGGACT---GAGGACCCACTTACCCAGATAGAGGACCCCA	315
Db	6209	CATAGTGAGAAGCTGAGGGAGAAGTCGGGAGGCCCTCTCCACCCAGATAGACGACCCCA	6268
Qy	316	AATAATCC-----CTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTCTCAGGC	366
Db	6269	AATAATCCGGCACCCCTCCTGCTTCCAGTCCTGGGCCACCCGTGGGCGGACTTCTGAGTC	6328
Qy	367	TGGGCCACCCCAAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAGCTCCGT	426
Db	6329	TGGGACGCCCACCACCCCACTGCCGCTGAAGCCGCAGGGACTATGGAGTCAGAGCTTGGT	6388
Qy	427	GTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACATCATGCT	486
Db	6389	GTGATCAGTGCAGGACTGGTGGGGT-----AGGCTCTGCCAGGCATCAACGT	6436
Qy	487	CAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAACCCCCAC	546
Db	6437	CAGGACCCTAGGAGAGGGCTGAGTGTCCCCCA---CCCCATTCTATCCCTACCCCTT	6493
Qy	547	TCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCAACCCAC	606
Db	6494	TCCCATCTGCACTCCC-----TACCCCATCTGTACCCCC	6527
Qy	607	ATCCCCCAACCCATCCCTCAACCCCTGATGCCCATCCGCCAGCCATTCCACCCCTCACCCC	666
Db	6528	ATTCCCCACCTGTGCCCCATCCTCCCCAACCCCAACCAGCCTCATACCCCTTCCCC	6587
Qy	667	CACCCCAACCCCAACGCCACTCCCAACCCCAACCCAGGCAGGATCCG-GTTCGCCAGG	725

Db	6588		CACCCCTACCTTCATCCCCATCAGTGCAGCATCCGGTTCACCCCTGCTTTCAATCCAGG	6647
Qy	726		AAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGAGAAGC	785
Db	6648		CAAGCCCTGGGTGGCCGGATGTGATGCCACTGACTTGTGAATTGAGGGTTAGAGAGAAGT	6707
Qy	786		GAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGGCTCTG	845
Db	6708		GAGTTTCTGGGTCTGAAGGGTGGC-TTGAGATCGGCAGAGGGAAGGTGGCCCAGGCTTTG	6766
Qy	846		TGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATAGAGAG	905
Db	6767		TGAAGAGGCAAAGTGAGACTCTGAGGGAGGATTGAGGAAACCCCTATCCCTGATAGAGGG	6826
Qy	906		CCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGACGTCT	965
Db	6827		TCCCAGCCCTGGACTACCC-----CGCGGAGGCTGACTTCT	6862
Qy	966		CAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTCTTCTC	1025
Db	6863		CAGACTGGGCTGCTCCCCACCTCCGCCCC-----TTCGCAACGCGTTTGTTTAAGCCAC	6917
Qy	1026		CCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAGG	1085
Db	6918		AGGGGACTCTGGAGTCAGAGGTTGGTGTGATCAGGGAAGGGCTGGTTAGGAGA-GGCATG	6976
Qy	1086		GCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAAG	1145
Db	6977		GCCCAGGCCCTGCCAGGAATCAAAGTCAGAAACC-TGAGAGGGAAGTGAAGTCCCCCAAG	7035
Qy	1146		ACTGCACTCCAATCCCCACTCCCACCCCATTGCGATTCCCATTCCCCACCCAACCCCCAT	1205
Db	7036		ATCCTAGTCTAACCCCACTCCCACAA-----	7062
Qy	1206		CTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACCACCT	1265
Db	7063		-----ATCCGCTGCCATTTGCTGCTCCATTTCCATTCTTTGCCCT	7104
Qy	1266		CCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCCAACCCAC	1325
Db	7105		CCACCCTACCA-----	7116
Qy	1326		CCTCATCTCTCATGTGCCCCACTCCCATCGCTCCCCATTCTGGCAGAATCCGGTTT	1385
Db	7117		-----GGCAGAATCCAGTTC	7131
Qy	1386		GCC-CCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACTTGAA	1444
Db	7132		CCCTTCTGCTATCAATCCAGGGAACCCAGGCTTGGTGTGGGATGTTTT-----	7183
Qy	1445		CCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAGATCC	1504
Db	7184		-----TGGGGGTCAGAGAATCAAGGGCATAGTCTGAGGGGCCAGTTGAGATCG	7232
Qy	1505		ACTGAGGGGAGTGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGGACTG	1564
Db	7233		GCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAGGCAAGGTGAGACTCTGAGGAAGGACTG	7292
Qy	1565		AGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTGCCAG	1624

Db 7293 AGGAGGCCCCACCCAAGATAGA-GGAACCCAAATAATCCAGCGCAGCTCCTGCTGCCAG 7351

Qy 1625 CCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCCCACT 1684
 ||||| ||||| || ||||| ||||| ||||| ||||| |||||

Db 7352 TCCTGGACCACCCGG---GGGAAGACTTCTCA----GGCTAGGCCATCCCAGCTCCCACT 7404

Qy 1685 GCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTTGGTC 1744
 ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7405 GCCACTAAAGCTACAGGGGACTCTAGAGTCAAGAGCTTGGTGTGCCCA----- 7452

Qy 1745 AGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGGACCC 1804
 ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7453 -----AGGCAGGGCCAGGC-----TCTGCCTGGCATCGGGGTCAGGACCT 7493

Qy 1805 TGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACCCAC 1864
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7494 TGAGAGGGAAC TGAGGGCGCTACACCCCAACCCATCCGCATTC-----CAACAT 7543

Qy 1865 TCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTGTCAA 1924
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7544 GCCCAGCCCCATCCCCAACTCCGTTTTGCAGAATCCATTTT-----TCCCTGCAGTCAA 7599

Qy 1925 CCCACGGAAGCCACGGGAATGGCGGCCAGGCATCGGATCTTGACGTCCCCATCCAGGGT 1984
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7600 CCCCAGGAAGACCTGGGAATGGT---CAGGCATCGGATCTTGACATCCACATCGAGGGC 7656

Qy 1985 CTGATGGAGGGAAGGGG-----CTTGAACAGGGCCTCAGGGGAGCAGAGGGAG----- 2032
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7657 TGAAGGAGGGAGAGGGTTTGGTATCATGAGCAGAGCCTCAGGGTAGCAGAGGGAGGACCC 7716

Qy 2033 -GGCCCTACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCC-----TAGGAC 2082
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7717 TGGCCCTCCTGGGAGATGAGGAAGGCCTCAGGAGACCCAGCACCCCAAGGCAGGGAGCCC 7776

Qy 2083 ACCGCACCCCTGTCTGAGACTGAG--GCTGCCACTTCTGGCCTCAAGAATCAGAACGATG 2140
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7777 ACCCCACCCCTGTCTGAGAATGAGGTGCCTCCTCTTTTAGCCTCAGGAATCCAAGGGATG 7836

Qy 2141 GGGACTCAGATTGCAT--GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAG 2198
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7837 GCAACTCAGGTCAGCAGAGGGGTGGGTTCGAAGCCCTTCCAGGATCAAGGAAAGGAAGAC 7896

Qy 2199 GAGGGAGGACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTC 2258
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7897 GAGGGAGGATTGAGGGGCGCTTGCATTCCAGATCAGTGGAGACCTGGGCGCTGGGAGGTC 7956

Qy 2259 CAGGGCACGGTGGCCACATATGGCCCATATTTCTGCATCTTTGAGGT----GACAGGAC 2314
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7957 CTGGGCAAGGTAGCCACCTGTAGCTCATACTTCTGCATCTTCGAGGTCACAGAGAGGAG 8016

Qy 2315 AGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTCCAGGATCCAT 2374
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 8017 AGGGCTATGGTCTGAGGGGTGGTACTTCAGGTCCGCAGAGGGAGGAGTCCAGGATCTAC 8076

Qy 2375 ATGGCCCAAGATGTGCC-CCCTTCATGAGGACTGGGGATATCCCGGCTCAGAAAGAAGG 2433
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 8077 AGGACCCAAGGTGTGCCACACTTCACGAGGAATGGGGATACCTGTGGCTCAGAAAGACGG 8136

Qy 2434 GACTCCACACAGTCTGGCTGTCCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGG 2493
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 8137 GACCCACAGAGTCTGGCTGTCCCCTGTTCTTAGCTCAGGGGGGACCAGAGGAGGGATGG 8196

Qy	2494	CGGTATGTTCCATTCTCACTTGTACCACAGGCAGGAAGTTGGGGGCCCTCAGGGAGATG	2553
Db	8197	CCCTATGTGCCAATTTCACTTGTTCACAGGCAGGAAGTTGGGGAACCTTCAGGGAGATG	8256
Qy	2554	GGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGTACAGGAATTGGGGGTTGAGGAAGCA	2613
Db	8257	AGGTTTGGAGTAAAGGGGCAATGTTTGCTCATCTCAGGGGTTGGGGGTTGAGGAAGGG	8316
Qy	2614	CAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCATTGGAATCCACACCCCA	2673
Db	8317	CAGGCCCTGTCAGGAGCAAACATGAGT-ACCCACAGGAGGCCATCAGAACCCTCACCCCA	8375
Qy	2674	GAACCAAAGGGGTGAGCCCTGGACACCTCACCCAG-----GATGTGGCTTCTTTTTTC	2725
Db	8376	GAACCAAAGGGGTGAGCCCTGGGCACCCACACAGGGGTGACAGGATGTGGCTCCTTCTC	8435
Qy	2726	ACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCTCATTCTCAGAGGGTGA CT CAGGTCA	2785
Db	8436	ATTTC TGATTCCAGATCTCAGTGAGGTGAGGACCTTGTTCTCAGAGGGTGACTCAGGTCA	8495
Qy	2786	ACGTAGGGGACCCCATCTGGTCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGG	2845
Db	8496	CCACAGGGGACCCCATCTGGTCTACAGACACAGTGGTCCCAGGATCTGCCAAGAGTCCTG	8555
Qy	2846	GTGAGGAACATGAGGGGAGGACTGAGGGTACCCAGGACCAGAACACTGAGGGGAGACTGCA	2905
Db	8556	GTGAGGAATGTGAGGGGAGGATTGAGGGTACCACAGGGCCAGAACGCAGATGATGACCCCA	8615
Qy	2906	CAGAAATCAGCCCTGCCCTGCTGTACCCAGAGAGCATGGGCTGGGCCGTCTGCCGAG	2965
Db	8616	CAGAAATCAGCCCTGCTCCTGTTGTCACCCAGAGAGCATGGGCTTGGCTTTCTGCTGAG	8675
Qy	2966	GTCCTTCGTTATCCTGGGATCATTGATGTCAGGGACGGGGAGGCCTTGGTCTGAGAAGG	3025
Db	8676	GTCCCTCTCTTATCCTGGGATCACTGGTGTACGGAGTGGGAGGCCTTGGTCTGAGGGGG	8735
Qy	3026	CTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCA	3085
Db	8736	CTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGGCTCTGCCAGGAGTTGAGGTGAGGACCA	8795
Qy	3086	AGCGGGCACCTCACCCAGGACACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCT	3145
Db	8796	AGCAGGCTCCGCATCCAGGACACATGGGTTCCAATGAATTTGACATCTTTTGCTGTCTGT	8855
Qy	3146	TC-CCCAAGGACCTAGGCACGTGTGGCCAGATGTTTGTCCCTCCTGTCCTTCCATTCCCT	3204
Db	8856	TCTTCGGAAGACCTAGGCACAGGTGGCCAGATGTGGGGTTTCTTAGGTCCT---GTTCCC	8912
Qy	3205	TATCATGGATGTGAACTCTTGATTGATTCTCAGACCAGCAAAAGGGCAGGATCCAGG	3264
Db	8913	TCTCAGGCATGTGAGCTCTTGATCTGAGTTCTCAGGCCAGCAAAAGAGTGGGATCCAGG	8972
Qy	3265	CCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGA	3324
Db	8973	CCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCCACTCCATGA	9032
Qy	3325	GAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGCCAGGGCTGT	3384
Db	9033	GAGTGGGGACCTCACAGAGTCCAGCCTACCCTCCTTGATGGCACTGAGGGACCGGGGCTGT	9092

Qy 3385 GCTTGC GG TCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCAGGAACCAGG 3444
 |||| | ||||||||| ||||| ||||||||| | ||||||||| |||
 Db 9093 GCTTACAGTCTGCACCCTAAGGGCCCATGGATTCTCTCTAGGAGCTCCAGGAACAAGG 9152

Qy 3445 CAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTG 3504
 ||||||||| ||||||| ||||||| ||||||| ||||||| ||||| |||
 Db 9153 CAGTGAGGCCTTGGTCTGAGACAGTGTCTCAGGTTACAGAGCAGAGGATGCACAGGCTG 9212

Qy 3505 TGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACA 3564
 ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||
 Db 9213 TGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAAGACACA 9272

Qy 3565 TAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAATCGACCTCTG 3624
 ||||||||| ||||||||| ||||||||| ||| ||||| ||||||||| |||
 Db 9273 TAGGACTCCAAAGAGTCTGGCCTCACCTCCCTACCATCAATCTGCAGAATCGACCTCTG 9332

Qy 3625 CTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCTCTCCTTCAGGTTTTCAGGGGACAGG 3683
 ||||||||| ||||||||| ||| ||||||||| ||||||||| ||| |||||
 Db 9333 CTGGCCGGCTATACCCTGAGGTGCTCTCTCACTTCTCTCCTTCAGGTTCTGAGCAGACAGG 9392

Qy 3684 CCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA 3743
 ||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||
 Db 9393 CCAACCG-GAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA 9451

Qy 3744 AGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACTTCTCAGCTGAGGCCTCTCACACACTCC 3803
 |||| ||||||||| ||| ||| ||| ||||||||| ||||||||| |||||
 Db 9452 AGTAAGCCTTTGTTAGAGCCTCTAAGATTGTTCTCAGCTGAGGTCTCTCACATGCTCC 9511

Qy 3804 CTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCTGCCTGCTG 3863
 ||||||||| ||||||||| ||||||||| ||||||||| ||||| ||||| |||||||||
 Db 9512 CTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCCAGCTTTTGCCTGCACTCTTGCCTGCTG 9571

Qy 3864 CCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAG 3923
 ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||
 Db 9572 CCCTGACCAGAGTCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAG 9631

Qy 3924 CCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCAC----- 3975
 | ||||||||| ||||||||| ||||||||| ||| ||||| |||
 Db 9632 GCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGGTGGGTGCACAGGCTCTACTACTGAGG 9691

Qy 3976 -----CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGC 4019
 ||||||||| ||||||||| ||||||||| |||||
 Db 9692 AGCAGGAGGCTGCTGTCTCCTCCTCCTCTGGTCCCTGGCACCCCTGGAGGAAGTGC 9751

Qy 4020 CCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTA 4079
 | ||||| |||| ||| ||||||||| ||||||||| ||||||||| |||||
 Db 9752 CTGCTGCTGAGTCAGCAGGTCTCCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCACTA 9811

Qy 4080 CCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGG 4139
 ||||||| ||||||| | ||||||||| ||||||||| ||||||||| |||||
 Db 9812 CCATCAGCTTCACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGG 9871

Qy 4140 GGCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGG 4199
 ||||||||| ||| | ||||||||| ||||| ||| ||| |||||
 Db 9872 GGCCAAGCACCTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGG 9931

Qy 4200 CTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAG 4259
 ||| |||| | ||||||||| ||||||||| ||||| |||||||||
 Db 9932 ATGAGTTGGCTCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAG 9991

Qy 4260 AAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAG 4319

Db	9992	 AAATGCTGGAGAGAGTCATCAAAAATTACAAGCGTGCTTTCCTGTGATCTTCGGCAAAG	10051
Qy	4320	CCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCCACCGGCC	4379
Db	10052	 CCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCCGCCAGCA	10111
Qy	4380	ACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATC	4439
Db	10112	 ACACCTACACCCTTGTCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAATC	10171
Qy	4440	AGATCATGCCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCG	4499
Db	10172	 AGATCTTTCCCAAGACAGGCCTTCTGATAATCGTCTGGGCACAATTGCAATGGAGGGCG	10231
Qy	4500	GCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGA	4559
Db	10232	 ACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGA	10291
Qy	4560	GGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAA	4619
Db	10292	 GGGAGCACACTGTCTATGGGGAGCCCAGGAACTGCTCACCCAAGATTTGGGTGCAGGAAA	10351
Qy	4620	AGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTTCCTGTGGG	4678
Db	10352	 ACTACCTGGAGTACCGGCAGGTACCGGCAGTAATCCTGCGCGCTATGAGTTTCCTGTGGG	10411
Qy	4679	GTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCA	4738
Db	10412	 GTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCA	10471
Qy	4739	GTGCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAG	4798
Db	10472	 ATGCAAGAGTTTCGATTGCGCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAG	10531
Qy	4799	AGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG----GGACTGGGCCAGTG	4854
Db	10532	 AGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCTGGGCCAGTG	10591
Qy	4855	CACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGTGTGACATGAGGCCCATTCCT	4914
Db	10592	 CATCTAACA--GCCCTGTGCAGCAGCTTCCCTTGCTCGTGTAAACATGAGGCCCATTCCT	10649
Qy	4915	CAC TC----TGAAGAGAGCGGTCAAGTGTCTCAGTAGTAGTTTCTGTTCTATTGGGTGA	4970
Db	10650	 CACTCTGTTTGAAGAAAATAGTCAGTGTCTTAGTAGTGGGTTTCTATTTTGTGGATGA	10709
Qy	4971	CTTGGAGATTTATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGG	5030
Db	10710	 CTTGGAGATTTATCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTTAATGGATGG	10768
Qy	5031	TTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATAT	5090
Db	10769	 TTGAATTAACCTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATAT	10828
Qy	5091	AGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAA	5150
Db	10829	 AGTTTAGGAGTAAGAGTCTTGTTTTTATTTCAGATTGGGAAATCCGTTCTATTTGTGAA	10888
Qy	5151	TTGGG---ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAA	5207

```

Db      10889 TTTGGGACATAATAACAGCAGTGGAGTAAGTATTTAGAAGTGTG---AATTCACCGTGAA 10945
Qy      5208 ATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAG 5267
      |||| ||||| ||||| ||||| ||||| ||||| |||||
Db      10946 ATAGGTGAGAT-----AAATTAAGATACTTAATCCCGCCTTATGCCTCAG 10993
Qy      5268 TCTATTCTGTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGA 5327
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      10994 TCTATTCTGTAAAATTTAAATATATATGCATACCTGGATTTCCTTGGCTTC---GTGA 11050
Qy      5328 ATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTC 5387
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      11051 ATGTAAGAGAAATTAATCTGAATAAATAATTCTTTCTGTTAACTGGCTCATTTCTTCTC 11110
Qy      5388 CATGCACTGAGCATCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGGTAA 5447
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      11111 TATGCACTGAGCATCTGCTCTGTGGAAGGCCAGGATTAGTAGTGAGATACTAGGGTAA 11170
Qy      5448 GCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAG 5507
      ||||| || ||| ||| ||||| || | || |||| |||| ||
Db      11171 GCCAGACACACCTACCGATAGGGTATTAAGAGTCTAGGAGCGCGGTACATATAATTAAG 11230
Qy      5508 GTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCT 5567
      ||| ||||| ||||| ||||| ||||| || || |||| |||||
Db      11231 GTGACAAGATGTCCTCTAAGATGTAGGGAAAAGT----AACGAGTGTGGGTATGGGGCT 11286
Qy      5568 CCGGGTGAGAGTGGTGGAGTGCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAAC 5627
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      11287 CCAGGTGAGAGTGGTCGGGTGTAAATTCCTGTG-TGGGGCCTTTGGGCTTTGGGAAAC 11345
Qy      5628 TGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
      |||| || ||||| |||| ||||| ||||| || |||| |||
Db      11346 TGCATTTTCTTCTGAGGGATCTGATTCTAATGAAGCTTGGTGGGTCC 11392

```

RESULT 14

HSU10687

LOCUS HSU10687 11495 bp DNA linear PRI 23-JUN-1995

DEFINITION Human MAGE-4a antigen (MAGE4a) gene, complete cds.

ACCESSION U10687

VERSION U10687.1 GI:533514

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 11495)

AUTHORS De Plaen,E., Arden,K., Traversari,C., Gaforio,J.J., Szikora,J.P.,
De Smet,C., Brasseur,F., van der Bruggen,P., Lethe,B.,
Lurquin,C.Brasseur.R., Chomez,P., De Backer,O., Cavenee,W. and
Boon,T.

TITLE Structure, chromosomal localization, and expression of 12 genes of
the MAGE family

JOURNAL Immunogenetics 40 (5), 360-369 (1994)

PUBMED 7927540

REFERENCE 2 (bases 1 to 11495)

AUTHORS De Plaen,E.

TITLE Direct Submission

JOURNAL Submitted (14-JUN-1994) Etienne De Plaen, Ludwig Institute for
Cancer Research, 74 Avenue Hippocrate, Brussels, 1200, Belgium

FEATURES	Location/Qualifiers
source	1. .11495 /organism="Homo sapiens" /mol_type="genomic DNA" /isolate="patient MZ2" /db_xref="taxon:9606" /chromosome="X" /sex="female" /cell_type="lymphocyte" /tissue_type="blood" /dev_stage="adult"
exon	450. .510 /note="exon 1-1"
exon	836. .937 /note="exon 1-2"
exon	1418. .1556 /note="exon 1-3"
exon	2108. .2246 /note="exon 1-4"
exon	2836. .2928 /note="exon 1-5"
exon	3508. .3607 /note="exon 1-6"
exon	4906. .4963 /note="exon 1-7"
exon	5519. .5648 /note="exon 1-8"
exon	9377. .9448 /number=2
exon	9524. .11091 /number=3
gene	9589. .10542 /gene="MAGE4a"
CDS	9589. .10542 /gene="MAGE4a" /codon_start=1 /product="MAGE-4a antigen" /protein_id="AAA68871.1" /db_xref="GI:533515" /translation="MSSEQKSHCKPEEGVEAQEEALGLVGAQAPTTEEQEA AVSSSS PLVPGTLEEVPAAESAGPPQSPQGASALPTTISFTCW RQPNEGSSSQEEEGPSTSPDA ESLFREALSNKVDELAHFLLRKYRAKELVTKAEMLERVIK NYKRCFPVIFGKASESLK MIFGIDVKEVDPASNTYTLVTCLGLSYDGLLGNNQIFPKTG LLIIVLGTIAMEGDSAS EEEIWEEELGVMGVYDGREHTVYGEPRKLLTQDWVQENYLEYRQVPGSNPARYEFLWGP RALAETSYVKVLEHVVRVNARVRIAYPSLREAALLEEEEGV"
polyA_signal	11072. .11077
polyA_site	11091
ORIGIN	

Query Match 46.8%; Score 2655; DB 5; Length 11495;
 Best Local Similarity 73.6%; Pred. No. 0;
 Matches 4231; Conservative 0; Mismatches 1100; Indels 416; Gaps 50;

Qy	21	CCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCCATCCAAACATCTTCACGCTC	80
Db	5969	CCAGCACCCCTATCCTCCCCAAACCCCACTACCTTATGTCTCATCCCCACCCCAAC	6028
Qy	81	ACCCCCAGCCCCAAGCCAGGCAGAAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAAGC-C	139
Db	6029	ACCACTATCCCCATCCAGGTTGAATCGCATTCGTTTCTGCTTTCAACCCAGGGAAGCTC	6088

QY	140	CAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGGTTAGAGAGAAGCGAGGTTT	199
Db	6089		
QY	200	CAGGTTCCCTGGATGTGATGCCAGTGACTTGTGCATTGGGGGTTAGAGAGACGCTAGCTTC	6148
QY	259	TCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGGCCCCA-GCTCTGTAAGGAGG	258
Db	6149		6208
QY	316	TCAGTCTGACAGGCAGCTTGGGATTGGCAGAGGGAAGCCGGTCCAGGCTCTGTGAGGTGG	6208
QY	367	CAAGGTGACATGCTGAGGGAGGACT---GAGGACCCACTTACCCAGATAGAGGACCCCA	315
Db	6209		6268
QY	427	CATAGTGAGAAGCTGAGGGAGAAGTCGGGAGGCCCTCTCCACCCAGATAGACGACCCCA	6268
QY	487	AATAATCC-----CTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTCTCAGGC	366
Db	6269		6328
QY	547	AATAATCCGGCACCCCTCTCTGCTTCCAGTCTGGGCCACCCGTGGGCGGACTTCTGAGTC	6328
QY	607	TGGGCCACCCCAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACATCATGCT	486
Db	6329		6388
QY	667	TGGGACGCCACCACCCCACTGCGCGTGAAGCCGAGGGACTATGGAGTCAGAGCTTGGT	6388
QY	726	GTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACATCATGCT	486
Db	6389		6436
QY	786	GTGATCAGTGCAGGACTGGTGGGGGT-----AGGCTCTGCCAGGCATCAACGT	6436
QY	846	CAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCCTGACCCAACCCCAAC	546
Db	6437		6493
QY	906	CAGGACCCTAGGAGAGGGCTGAGTGTCCCCA---CCCCATTCTATCCCCTACCCCTT	6493
QY	966	TCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTTCATTCCAACCCCAACCCCAAC	606
Db	6494		6527
QY	1026	TCCCATCTGCACTCCC-----TACCCCATCTGTACCCCC	6527
QY	1086	ATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCTCACCCC	666
Db	6528		6587
QY	1146	ATTCCCCACCTGTGCCCCCTATCTCCCCAACCCCCAACCCAGCCTCATACCCCCCTCCCC	6587
QY	1206	CACCCCCACCCCAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACATCATGCT	725
Db	6588		6647
QY	1266	CACCCCTACCTTCATCCCCATCAGTGCAGCATCCGGTTCACCCCTGCTTTCAATCCAGG	6647
QY	1326	AAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTTGTGGGGCAGAGAGAAGC	785
Db	6648		6707
QY	1386	CAAGCCCTGGGTGGCCGGATGTGATGCCACTGACTTGTGAATTGAGGGTTAGAGAGAAGT	6707
QY	1446	GAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGGCTCTG	845
Db	6708		6766
QY	1506	GAGTTTCTGGGTCTGAAGGGTGGC-TTGAGATCGGCAGAGGGAAGGTGGCCAGGCTTTG	6766
QY	1566	TGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATAGAGAG	905
Db	6767		6826
QY	1626	TGAAGAGGCAAGGTGAGACTCTGAGGGAGGATTTCAGGAAACCCCTATCCCTGATAGAGGG	6826
QY	1686	CCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAGACGTCT	965
Db	6827		6862
QY	1746	TCCCAGCCCTGGACTACCC-----CGCGGAGGCTGACTTCT	6862
QY	1806	CAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTCTTCTC	1025
Db	6863		6917
QY	1866	CAGACTGGGCTGCTCCCCACCTCCGCCCC-----TTCGCAACGCGTTTGTTTAAGCCAC	6917
QY	1926	CCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAGG	1085

Db	6918	AGGGGACTCTGGAGTCAGAGGTTGGTGTGATCAGGGAAGGGCTGGTTAGGAGA-GGCATG	6976
Qy	1086	GCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAAG	1145
Db	6977	GCCCAGGCCCTGCCAGGAATCAAAGTCAGAAACC-TGAGAGGGAAGTGGAGTCCCCCAAG	7035
Qy	1146	ACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACCCCAT	1205
Db	7036	ATCCTAGTCTAACCCCTACTCCACAA-----	7062
Qy	1206	CTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACCACCT	1265
Db	7063	-----ATCCGCTGCCATTTGCTGCTCCATTTCCCATTCCTTGCCCT	7104
Qy	1266	CCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCCAACCCAC	1325
Db	7105	CCACCCTACCA-----	7116
Qy	1326	CCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCCGGTTT	1385
Db	7117	-----GGCAGAATCCAGTTC	7131
Qy	1386	GCC-CCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACTTGAA	1444
Db	7132	CCCTTCTGCTATCAATCCAGGGAACCCAGGCTTGGTGTGGGATGTTTT-----	7183
Qy	1445	CCTCACAGATCTGAGAGAAGCCAGGTTCAATTTAATGGTTCTGAGGGGCGGCTTGAGATCC	1504
Db	7184	-----TGGGGGTCAGAGAATCAAGGGCATAGTCCTGAGGGGCCAGTTGAGATCG	7232
Qy	1505	ACTGAGGGGAGTGTTTGGTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGGACTG	1564
Db	7233	GCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAGGCAAGGTGAGACTCTGAGGAAGGACTG	7292
Qy	1565	AGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTGCCAG	1624
Db	7293	AGGAGGCCCCACCCAAGATAGA-GGAACCCAAATAATCCAGCGAGCTCCTGCTGCCAG	7351
Qy	1625	CCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCCCACT	1684
Db	7352	TCCTGGACCACCCGG--GGGAAGACTTCTCA---GGCTAGGCCATCCAGCTCCCACT	7404
Qy	1685	GCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGCAGGGTTGGTC	1744
Db	7405	GCCACTAAAGCTACAGGGGACTCTAGAGTCAAGAGCTTGGTGTGCCCA-----	7452
Qy	1745	AGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCAGCATAGGGTCAGGACCC	1804
Db	7453	-----AGGCAGGGCCAGGC-----TCTGCCTGGCATCGGGGTCAGGACCT	7493
Qy	1805	TGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACCCAC	1864
Db	7494	TGAGAGGGAAGTGAAGGCGCTACACCCCAACCCATCCGCATC-----CAACAT	7543
Qy	1865	TCACATTCCCATACTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTGTCAA	1924
Db	7544	GCCCAGCCCCATCCCCAATCCGTTTTGCAGAATCCATTTT-----TCCCTGTCAGTCAA	7599
Qy	1925	CCCACGGAAGCCACGGAATGGCGGCCAGGCATCGGATCTTGACGTCCCCATCCAGGGT	1984

Db	7600	CCCCGGGAAGACCTGGGAATGGT---CAGGCACTCGGATCTTGACATCCACATCGAGGGC	7656
Qy	1985	CTGATGGAGGGAAGGGG-----CTTGAACAGGGCCTCAGGGGAGCAGAGGGAG-----	2032
Db	7657	TGAAGGAGGGAGAGGGTTTGGTATCATGAGCAGAGCCTCAGGGTAGCAGAGGGAGGACCC	7716
Qy	2033	-GGCCCTACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCC-----TAGGAC	2082
Db	7717	TGGCCCTCCTGGGAGATGAGGAAGGCCTCAGGAGACCCAGCACCCAAGGCAGGGAGCCC	7776
Qy	2083	ACCGCACCCCTGTCTGAGACTGAG--GCTGCCACTTCTGGCCTCAAGAATCAGAACGATG	2140
Db	7777	ACCCACCCCTGTCTGAGAATGAGGTGCCTCCTCTTTTAGCCTCAGGAATCCAAGGGATG	7836
Qy	2141	GGGACTCAGATTGCAT--GGGGGTGGGACCAGGCCTGCAAGGCTTACGCGGAGGAAGAG	2198
Db	7837	GCAACTCAGGTCAGCAGAGGGGTGGGTTC AAGCCCTTCCAGGATCAAGGAAAGGAAGAC	7896
Qy	2199	GAGGGAGGACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTC	2258
Db	7897	GAGGGAGGATTCAGGGGGCCTTGCATTCAGATCAGTGGAGACCTGGGCCCTGGGAGGTC	7956
Qy	2259	CAGGGCACGGTGGCCACATATGGCCCATATTTCTGCATCTTTGAGGT---GACAGGAC	2314
Db	7957	CTGGGCAAGGTAGCCACCTGTAGCTCATACTTCTGCATCTTCGAGGTCACAGAGAGGAG	8016
Qy	2315	AGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCAGGATCCAT	2374
Db	8017	AGGGCTATGGTCTGAGGGGTGGTACTTCAGGTCCGCAGAGGGAGGAGTCCAGGATCTAC	8076
Qy	2375	ATGGCCCAAGATGTGCC-CCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAAGAGG	2433
Db	8077	AGGACCCAAGGTGTGCCACACTTCACGAGGAATGGGGATACCTGTGGCTCAGAAAGACGG	8136
Qy	2434	GACTCCACACAGTCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGG	2493
Db	8137	GACCCACACAGTCTGGCTGTCCCTGTTCCTTAGCTCAGGGGGGACCAGAGGAGGGATGG	8196
Qy	2494	CGGTATGTTCCATTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATG	2553
Db	8197	CCCTATGTGCCAATTTCACTTGTTCACAGGCAGGAAGTTGGGGAACCTTCAGGGAGATG	8256
Qy	2554	GGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGT CAGGGAATTGGGGGTTGAGGAAGCA	2613
Db	8257	AGGTTTTGGAGTAAAGGGGCAATGTTTGCTCATCTCAGGGGGTTGGGGGTTGAGGAAGGG	8316
Qy	2614	CAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCCA	2673
Db	8317	CAGGCCCTGTCAGGAGCAAACATGAGT-ACCCACAGGAGGCCATCAGAACCCCTCACCCCA	8375
Qy	2674	GAACCAAAGGGGTGAGCCCTGGACACCTCACCCAG-----GATGTGGCTTCTTTTTTC	2725
Db	8376	GAACCAAAGGGGTGAGCCCTGGGCACCCACACAGGGGTGACAGGATGTGGCTCCTTCTC	8435
Qy	2726	ACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCTCATTTCTCAGAGGTTGACTCAGGTCA	2785
Db	8436	ATTTCTGATTCCAGATCTCAGTGAGGTGAGGACCTTGTTCTCAGAGGTTGACTCAGGTCA	8495
Qy	2786	ACGTAGGGACCCCATCTGGTCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGG	2845
Db	8496	CCACAGGGACCCCATCTGGTCTACAGACACAGTGGTCCCAGGATCTGCCAAGAGTCCTG	8555

Qy	2846	GTGAGGAACATGAGGGAGGACTGAGGGTACCCAGGACCAGAACTGAGGGAGACTGCA	2905
Db	8556	GTGAGGAATGTGAGGGAGGATTGAGGGTACCACAGGGCCAGAACGCAGATGATGACCCCA	8615
Qy	2906	CAGAAATCAGCCCTGCCCCCTGCTGTACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAG	2965
Db	8616	CAGAAATCAGCCCTGCTCCTGTGTGTACCCCAGAGAGCATGGGCTTGGCTTTCTGCTGAG	8675
Qy	2966	GTCCTTCCGTTATCCTGGGATCATTGATGTCAGGGACGGGGAGGCCTTGGTCTGAGAAGG	3025
Db	8676	GTCCCTCTCTTATCCTGGGATCACTGGTGTACGGAGTGGGAGGCCTTGGTCTGAGGGGG	8735
Qy	3026	CTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCA	3085
Db	8736	CTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGGCTCTGCCAGGAGTTGAGGTGAGGACCA	8795
Qy	3086	AGCGGGCACCTCACCCAGGACACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCT	3145
Db	8796	AGCAGGCTCCGCATCCAGGACACATGGGTTCGAATTCGACATCTTTTGCTGTCGT	8855
Qy	3146	TC-CCCAAGGACCTAGGCACGTGTGGCCAGATGTTTGTCCCCTCCTGTCCTTCCATTCCCT	3204
Db	8856	TCTTCGGAAGACCTAGGCACAGGTGGCCAGATGTGGGGTTTCTTAGGTCCT---GTTCCC	8912
Qy	3205	TATCATGGATGTGAACTCTTGATTTGGATTTCTCAGACCAGCAAAAGGGCAGGATCCAGG	3264
Db	8913	TCTCAGGCATGTGAGCTCTTGATCTGAGTTTCTCAGGCCAGCAAAAGAGTGGGATCCAGG	8972
Qy	3265	CCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGA	3324
Db	8973	CCCTGCCCTGGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCCACTCCATGA	9032
Qy	3325	GAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGCCAGGGCTGT	3384
Db	9033	GAGTGGGGACCTCACAGAGTCCAGCCTACCCTCTTGATGGCACTGAGGGACCGGGGCTGT	9092
Qy	3385	GCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTCCTGGAGCTCCAGGAACCAGG	3444
Db	9093	GCTTACAGTCTGCACCCTAAGGGCCCATGGATTCTCTCCTAGGAGCTCCAGGAACAAGG	9152
Qy	3445	CAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTG	3504
Db	9153	CAGTGAGGCCTTGGTCTGAGACAGTGTCTCCTCAGGTTACAGAGCAGAGGATGCACAGGCTG	9212
Qy	3505	TGCCAGCAGTGAATGTTTGCCTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACA	3564
Db	9213	TGCCAGCAGTGAATGTTTGCCTGAATGCACACCAAGGGCCCCACCTGCCACAAGACACA	9272
Qy	3565	TAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAATCGACCTCTG	3624
Db	9273	TAGGACTCCAAAGAGTCTGGCCTCACCTCCCTACCATCAATCCTGCAGAATCGACCTCTG	9332
Qy	3625	CTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTTCAGGTTTTCAGGGGACAGG	3683
Db	9333	CTGGCCGGCTATACCCTGAGGTGCTCTCTCACTTCCTCCTTCAGGTTCTGAGCAGACAGG	9392
Qy	3684	CCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAAGATCTGTA	3743
Db	9393	CCAACCG-GAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAAGATCTGTA	9451

Qy	3744	AGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCC	3803
Db	9452	AGTAAGCCTTTGTTAGAGCCTCTAAGATTTGGTTCTCAGCTGAGGTCTCTCACATGCTCC	9511
Qy	3804	CTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCTGCCTGCTG	3863
Db	9512	CTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCCAGCTTTTGCCTGCACTCTTGCTGCTG	9571
Qy	3864	CCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAG	3923
Db	9572	CCCTGACCAGAGTCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAG	9631
Qy	3924	CCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC-----	3975
Db	9632	GCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGGTGGGTGCACAGGCTCCTACTACTGAGG	9691
Qy	3976	-----CTCCTCCTCCTCTCCTCTGGTCCCTGGGCACCCTGGAGGAGGTGC	4019
Db	9692	AGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTCTGGTCCCTGGCACCCTGGAGGAAGTGC	9751
Qy	4020	CCACTGCTGGGTCAACAGATCCTCCCCAGAGTCTCAGGGAGCCTCCGCCTTTCCCCTA	4079
Db	9752	CTGCTGCTGAGTCAGCAGGTCTCCTCCCCAGAGTCTCAGGGAGCCTCTGCCTTACCCCTA	9811
Qy	4080	CCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGG	4139
Db	9812	CCATCAGCTTCACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGG	9871
Qy	4140	GGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGG	4199
Db	9872	GGCCAAGCACCTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGG	9931
Qy	4200	CTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAG	4259
Db	9932	ATGAGTTGGCTCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAG	9991
Qy	4260	AAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAG	4319
Db	9992	AAATGCTGGAGAGAGTATCAAAAATTACAAGCGCTGCTTTCTGTGATCTTCGGCAAAG	10051
Qy	4320	CCTCTGAGTCCTTGCACTGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCC	4379
Db	10052	CCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGACCCCGCCAGCA	10111
Qy	4380	ACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATC	4439
Db	10112	ACACCTACACCTTGTACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAATC	10171
Qy	4440	AGATCATGCCCAAGACAGGCTTCTTGATAATTGTCTGGTCATGATTGCAATGGAGGGCG	4499
Db	10172	AGATCTTTCCCAAGACAGGCTTCTTGATAATCGTCTGGGCACAATTGCAATGGAGGGCG	10231
Qy	4500	GCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGA	4559
Db	10232	ACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGA	10291
Qy	4560	GGGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAA	4619
Db	10292	GGGAGCACACTGTCTATGGGGAGCCCAGGAACTGCTCACCCAAGATTTGGTGCAGGAAA	10351
Qy	4620	AGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGG	4678

Db	10352	ACTACCTGGAGTACCGGCAGGTACCCGGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGG	10411
Qy	4679	GTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCA	4738
Db	10412	GTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCA	10471
Qy	4739	GTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAG	4798
Db	10472	ATGCAAGAGTTCGCATTGCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAG	10531
Qy	4799	AGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG----GGACTGGGCCAGTG	4854
Db	10532	AGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTGTGGGAAGGGGCAGGGCTGGGCCAGTG	10591
Qy	4855	CACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCGTGTGACATGAGGCCCATTTCTT	4914
Db	10592	CATCTAACA--GCCCTGTGCAGCAGCTTCCCTTGCGTGTAAACATGAGGCCCATTTCTT	10649
Qy	4915	CACTC----TGAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGA	4970
Db	10650	CACTCTGTTTGAAGAAAATAGTCAGTGTTCTTAGTAGTGGGTTTCTATTTGTTGGATGA	10709
Qy	4971	CTTGGAGATTTATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGG	5030
Db	10710	CTTGGAGATTTATCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTTAATGGATGG	10768
Qy	5031	TTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATAT	5090
Db	10769	TTGAATTAAC TTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATAT	10828
Qy	5091	AGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTGTGAA	5150
Db	10829	AGTTTAGGAGTAAGAGTCTTGTTTTTTATTTCAGATTGGGAAATCCGTCTATTTGTGAA	10888
Qy	5151	TTGGG---ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAA	5207
Db	10889	TTTGGGACATAATAACAGCAGTGGAGTAAGTATTTAGAAGTGTG---AATTCACCGTGAA	10945
Qy	5208	ATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAG	5267
Db	10946	ATAGGTGAGAT-----AAATTAAGATACTTAATTCCCGCCTTATGCCTCAG	10993
Qy	5268	TCTATTCTGTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGCTTCTTTGAGA	5327
Db	10994	TCTATTCTGTAAAATTTAAAAATATATATGCATACCTGGATTTCCTTGCTTC---GTGA	11050
Qy	5328	ATGTAAGAGAAATTAATCTGAATAAAGAAATTCCTTCTGTTCACTGGCTCTTTTCTTCTC	5387
Db	11051	ATGTAAGAGAAATTAATCTGAATAAATAATTCTTTCTGTTAACTGGCTCATTTCTTCTC	11110
Qy	5388	CATGCACTGAGCATCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAA	5447
Db	11111	TATGCACTGAGCATCTGCTCTGTGGAAGGCCCAGGATTAGTAGTGGAGATACTAGGGTAA	11170
Qy	5448	GCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAG	5507
Db	11171	GCCAGACACACACCTACCGATAGGGTATTAAGAGTCTAGGAGCGCGTCAATAATTAAG	11230
Qy	5508	GTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCT	5567

```

Db      11231 GTGACAAGATGTCCTCTAAGATGTAGGGGAAAAGT----AACGAGTGTGGGTATGGGGCT 11286
Qy      5568 CCGGGTGAGAGTGGTGGAGTGTCATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAAC 5627
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      11287 CCAGGTGAGAGTGGTCGGGTGTAAATTCCTGTG-TGGGGCCTTTTGGGCTTTGGGAAAC 11345
Qy      5628 TGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        |||| || ||||| |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      11346 TGCATTTTCTTCTGAGGGATCTGATTCTAATGAAGCTTGGTGGGTCC 11392

```

RESULT 15

U82696

LOCUS U82696 161664 bp DNA linear PRI 31-DEC-2002

DEFINITION Homo sapiens chromosome X clone ICRFXc104-F064, ICRFXc104-G0799, Qc-14E2, Qc-13D8, Qc-7G11, ICRFXc104-E0681, Qc-11C8, Qc-9A9 map q28, complete sequence.

ACCESSION U82696

VERSION U82696.2 GI:27436770

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 161664)

AUTHORS Galgoczy, P., Wen, G. and Platzner, M.

TITLE Chromosome X genomic sequence

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 161664)

AUTHORS Gloeckner, G., Rosenthal, A., Drescher, B., Schattevoy, R., Hinzmann, B. and Poustka, A.

TITLE Direct Submission

JOURNAL Submitted (19-DEC-1996) Genome Analysis, Institut for Molecular Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany

REFERENCE 3 (bases 1 to 161664)

AUTHORS Platzner, M.

TITLE Direct Submission

JOURNAL Submitted (31-DEC-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany

COMMENT On Dec 31, 2002 this sequence version replaced gi:2735037.

----- Genome Center

Center: Insitute of Molecular Biotechnology

Center code: IMB

Web site: <http://genome.imb-jena.de/>

Contact: gscj-submit@genome.imb-jena.de

----- Project Information

Center project name: x81+

Center clone name: ICRFXc104-F064 to Qc-9A9

----- Summary Statistics

Sequencing vector: M13 and pUC18; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 161664 bases at least Q40

Consensus quality: 161664 bases at least Q30

Consensus quality: 161664 bases at least Q20

Quality coverage: 26.71x

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone.

 Neighboring sequence information:

This clone is overlapped by RP11-366F6, RP1-228J9, RP1-77B24, RP1-73F14.

 Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

```

FEATURES             Location/Qualifiers
     source            1. .161664
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /chromosome="X"
                        /map="q28"
                        /clone="ICRFxc104-F064, ICRFXc104-G0799, Qc-14E2, Qc-13D8,
                        Qc-7G11, ICRFXc104-E0681, Qc-11C8, Qc-9A9"
     source            1. .39145
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /clone="ICRFxc104-F064"
                        /clone_lib="ICRF human X specific cosmid library no.104"
     source            1. .46826
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /clone="RP1-228J9"
                        /clone_lib="RPCI human PAC 1"
                        /note="overlapping clone"
     source            1. .144241
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /clone="RP11-366F6"
                        /clone_lib="RPCI human BAC 11"
                        /note="overlapping clone"
     source            15197. .60086
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /clone="ICRFxc104-G0799"
                        /clone_lib="ICRF human X specific cosmid library no.104"
     source            47833. .85228
                        /organism="Homo sapiens"
                        /mol_type="genomic DNA"
                        /db_xref="taxon:9606"
                        /clone="Qc-14E2_A"
                        /clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
     source            51142. .89908
                        /organism="Homo sapiens"

```

```

source      /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="Qc-13D8"
            /clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
            79784. .117526
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="Qc-7G11"
            /clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
source      83247. .161664
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="RP1-77B24"
            /clone_lib="RPCI human PAC 1"
            /note="overlapping clone"
source      90591. .127521
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="ICRFxc104-E0681"
            /clone_lib="ICRF human X specific cosmid library no.104"
source      97402. .138230
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="Qc-11C8"
            /clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
source      125957. .161664
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="Qc-9A9"
            /clone_lib="QIZ-derived Xq27.3-Xqter cosmid library"
source      153955. .161664
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="RP1-73F14"
            /clone_lib="RPCI human PAC 1"
            /note="overlapping clone"
variation    114
            /note="C substituted in clone: RP11-366F6"
            /replace="a"
variation    205
            /note="deleted in clone: RP1-228J9 , deleted in clone:
            ICRFXc104-F064"
            /replace=""
variation    355
            /note="T substituted in clone: RP11-366F6"
            /replace="c"
variation    403
            /note="T substituted in clone: RP11-366F6"
            /replace="g"
misc_feature 485. .642
            /note="single stranded/single chemistry region"
variation    601
            /note="T substituted in clone: RP11-366F6"
            /replace="c"
variation    1040

```

```

variation    /note="C substituted in clone: RP11-366F6"
              /replace="t"
              1080
variation    /note="C substituted in clone: RP11-366F6"
              /replace="t"
              1760
variation    /note="A substituted in clone: RP11-366F6"
              /replace="g"
              2138
variation    /note="C substituted in clone: RP11-366F6"
              /replace="g"
              2298
variation    /note="C substituted in clone: RP11-366F6"
              /replace="t"
              2474. .2475
variation    /note="TT substituted in clone: RP11-366F6"
              /replace="aa"
              2515
variation    /note="G substituted in clone: RP11-366F6"
              /replace="a"
              2531
variation    /note="C substituted in clone: RP11-366F6"
              /replace="t"
              2691
variation    /note="A substituted in clone: RP11-366F6"
              /replace="g"
              2808
variation    /note="C substituted in clone: RP11-366F6"
              /replace="t"
              3334

```

Query Match 46.8%; Score 2654.8; DB 5; Length 161664;
 Best Local Similarity 73.6%; Pred. No. 0;
 Matches 4231; Conservative 0; Mismatches 1102; Indels 415; Gaps 50;

```

Qy      21 CCTCCCCCTACCACCCCCAATCCCTCCCTTTACGCCACCCATCCAAACATCTTCACGCTC 80
      || || || || || || || || || || || || || || || || || || || || || ||
Db      60227 CCAGCACCCCTATCCTCCCCAAACCCCCACTACCCTTATGTCCTCATCCCCACCCCAAC 60286

Qy      81 ACCCCCAGCCCCAAGCCAGGCAGAAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAAGC-C 139
      ||| || || || || || || || || || || || || || || || || || || || || ||
Db      60287 ACCACTATCCCCATCCAGGTTGAATCGCATTCGTTTCTGCTTTCACCCAGGGAAGCTC 60346

Qy      140 CAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGGTTAGAGAGAAGCGAGGTTT 199
      |||| || || || || || || || || || || || || || || || || || || || ||
Db      60347 CAGGTTCCTGATGTGATGCCAGTGACTTGTGCATTGGGGGTTAGAGAGACGCTAGCTTC 60406

Qy      200 TCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGGCCCA-GCTCTGTAAGGAGG 258
      || || || || || || || || || || || || || || || || || || || || || ||
Db      60407 TCAGTCTGACAGGCAGCTTGGGATTGGCAGAGGGAAGCCGGTCCAGGCTCTGTGAGGTGG 60466

Qy      259 CAAGGTGACATGCTGAGGGAGGACT---GAGGACCCACTTACCCAGATAGAGGACCCCA 315
      || || || || || || || || || || || || || || || || || || || || || ||
Db      60467 CATAGTGAGAAGCTGAGGGAGAAGTCGGGAGGCCCTCTCCACCCAGATAGACGACCCCA 60526

Qy      316 AATAATCC-----CTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTCTCAGGC 366
      |||| || || || || || || || || || || || || || || || || || || || ||
Db      60527 AATAATCCGGCACCCCTCCTGCTTCCAGTCCTGGGCCACCCGTGGGCGGACTTCTGAGTC 60586

Qy      367 TGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTC-GAAGTCAGAGCTCCG 425
      |||| || || || || || || || || || || || || || || || || || || || ||

```

Db 60587 TGGGACGCCACCACCCCACTGCCGCTGAAGCCGCAGGGGACTATGGAGTCAGAGCTTGG 60646

Qy 426 TGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACATCATGC 485
 ||||| ||| ||| ||| ||| ||||| |||||

Db 60647 TGTGATCAGTGCAGGACTGGTGGGGGT-----AGGCTCTGCCAGGCATCAACG 60694

Qy 486 TCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAACCCCCA 545
 ||||| || ||||| ||||| ||||| ||| ||| ||| |||||

Db 60695 TCAGGACCCTAGGAGAGGGCTGAGTGTCCCCA---CCCCATTCCTATCCCCTACCCCT 60751

Qy 546 CTCCAATGCTCACTCCCGTGACCCAACCCCCTCTTCATTGTCAATTCCAACCCCCACCCA 605
 ||| || ||||| ||||| ||||| ||| ||| |||

Db 60752 TTCCCATCTGCACTCCC-----TACCCCATCTGTACCCC 60785

Qy 606 CATCCCCACCCCATCCCTCAACCCTGATGCCATCCGCCAGCCATTCCACCCTCACCC 665
 ||| ||||| ||| ||| ||| ||| ||| ||||| ||||| |||||

Db 60786 CATTCCCACCTGTGCCCTATCTCCCCAACCCCCCAACCAGCTCATACCCCCCTCCC 60845

Qy 666 CCACCCCCACCCCAACGCCCACTCCCAACCCCCACCCAGGCAGGATCCG-GTTCCCGCCAG 724
 ||||| ||| || ||||| ||| ||| ||| ||| ||| |||||

Db 60846 CCACCCCTACCTTCATCCCCATCAGCGCAGCATCCGGTTCACCCCTGCTTTCAATCCAG 60905

Qy 725 GAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGAGAAG 784
 ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 60906 GCAAGCCCTGGGTGGCCGGATGTGATGCCACTGACTTGTGAATTGAGGGTTAGAGAGAAG 60965

Qy 785 CGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGGCTCT 844
 ||| || ||||| || ||| ||| ||||| || ||||| || ||||| ||

Db 60966 TGAGTTTCTGGGTCTGAAGGGTGGC-TTGAATCGGCAGAGGGAAGGTGGCCCAGGCTTT 61024

Qy 845 GTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATAGAGA 904
 |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61025 GTGAAGAGGCAAAGTGAGACTCTGAGGGAGGATTGAGGAAACCCCTATCCCTGATAGAGG 61084

Qy 905 GCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGACGTC 964
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61085 GTCCCAGCCCTGGACTACCC-----CGCGGAGGCTGACTTC 61120

Qy 965 TCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAGCCTTGAGAGACACCAGGTTCTTCT 1024
 |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61121 TCAGACTGGGCTGCTCCCCACCTCCGCCCC-----TTCGCAACGCGTTTGTTTAAGCCA 61175

Qy 1025 CCCCAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAG 1084
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61176 CAGGGGACTCTGGAGTCAGAGGTTGGTGTGATCAGGGAAGGGCTGGTTAGGAGAGGGCAT 61235

Qy 1085 GGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAA 1144
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61236 GGCCCAGGCCCTGCCAGGAATCAAGTCAGAAACC-TGAGAGGGAAGTGGTCCCCCAA 61294

Qy 1145 GACTGCACTCCAATCCCCACTCCCACCCATTGCGATTCCCATCCCCACCCAACCCCCA 1204
 || ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61295 GATCCTAGTCTAACCCCCACTCCCACA----- 61321

Qy 1205 TCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACCACCC 1264
 |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61322 -----AATCCGCTGCCATTTGCTGCTCCATTTCCCATTCCTTGCCC 61363

Qy 1265 TCCAGCCCCAGCACCCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAACCCCCA 1324
 |||| || ||||

Db 61364 TCCACCCTCACCA----- 61376

Qy 1325 CCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTTGGCAGAATCCGGTT 1384
 Db 61377 -----GGCAGAATCCAGTT 61390
 Qy 1385 TGCC-CCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACTTGA 1443
 Db 61391 CCCCTTCTGCTATCAATCCAGGGAAACCCAGGCTTGGTGTGGGATGTTTTT----- 61443
 Qy 1444 ACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGAGATC 1503
 Db 61444 -----TGGGGGTCAGAGAATCAAGGGCATAGTCTGAGGGGCCAGTTGAGATC 61491
 Qy 1504 CACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGGACT 1563
 Db 61492 GGCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAGGCAAGGTGAGACTCTGAGGAAGGACT 61551
 Qy 1564 GAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTGCCA 1623
 Db 61552 GAGGAGGCCCCACCCAAGATAGA-GGAACCCAAATAATCCAGCGCAGCTCCTGCTGCCA 61610
 Qy 1624 GCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCCCAC 1683
 Db 61611 GTCCTGGACCACCCGG---GGGAAGACTTCTCA----GGCTAGGCCATCCCAGCTCCCAC 61663
 Qy 1684 TGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTTGGT 1743
 Db 61664 TGCCACTAAAGCTACAGGGGACTCTAGAGTCAAGAGCTTGGTGTGCCCA----- 61712
 Qy 1744 CAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGGACC 1803
 Db 61713 -----AGGCAGGGCCCAGGC-----TCTGCCTGGCATCGGGGTAGGACC 61752
 Qy 1804 CTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACCCCA 1863
 Db 61753 TTGAGAGGGAAC TGAGGGCGCTACACCCCAACCCATCCGCATTC-----CAACA 61802
 Qy 1864 CTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTGTCA 1923
 Db 61803 TGCCCAGCCCCATCCCAACTCCGTTTGCAGAATCCATTTT-----TCCCCTGCAGTCA 61858
 Qy 1924 ACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCAGGG 1983
 Db 61859 ACCCCGGGAAGACCTGGGAATGGT---CAGGCACTCGGATCTTGACATCCACATCGAGGG 61915
 Qy 1984 TCTGATGGAGGGAAGGG-----GCTTGAACAGGGCCTCAGGGGAGCAGAGGGAG---- 2032
 Db 61916 CTGAAGGAGGGAGAGGGTTTGGTATCATGAGCAGAGCCTCAGGGTAGCAGAGGGAGGACC 61975
 Qy 2033 --GGCCCTACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCCTAGGACACCG---- 2086
 Db 61976 CTGGCCCTCCTGGGAGATGAGGAAGGCCTCAGGAGACCCAGCACCCCAAGGCAGGGAGCC 62035
 Qy 2087 ----CACCCCTGTCTGAGACTGAG--GCTGCCACTTCTGGCCTCAAGAATCAGAACGATG 2140
 Db 62036 CACCCACCCCGTCTGAGAATGAGGTGCCTCCTCTTTTAGCCTCAGGAATCCAAGGGATG 62095
 Qy 2141 GGGACTCAGATTGCATGGGGGTGGGA--CCCAGGCCTGCAAGGCTTACGCGGAGGAAGAG 2198
 Db 62096 GCAACTCAGGTCAGCAGAGGGGTGGGTTCAGGCCCTTCCAGGATCAAGGAAAGGAAGAC 62155

Qy	2199	GAGGGAGGACTCAGGGGACCTTGGAAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTC	2258
Db	62156		
		GAGGGAGGATTTCAGGGGACCTTGCATTCCAGATCAGTGGAGACCTGGGCCCTGGGAGGTC	62215
Qy	2259	CAGGGCACGGTGGCCACATATGGCCCATATTTCTGCATCTTTGAGGT----GACAGGAC	2314
Db	62216		
		CTGGGCAAGGTAGCCACCTGTAGCTCATACTTCTGCATCTTCGAGGTCACAGAGAGGAG	62275
Qy	2315	AGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCAT	2374
Db	62276		
		AGGGCTATGGTCTGAGGGTGGTACTTCAGGTCCGCAGAGGGAGGAGTCCCAGGATCTAC	62335
Qy	2375	ATGGCCCAAGATGTGCC--CCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGG	2433
Db	62336		
		AGGACCCAAGGTGTGCCACACTTCACGAGGAATGGGGATACCTGTGGCTCAGAAAGACGG	62395
Qy	2434	GACTCCACACAGTCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGG	2493
Db	62396		
		GACCCACAGAGTCTGGCTGTCCCTGTTCTTAGCTCAGGGGGACCAGAGGAGGGATGG	62455
Qy	2494	CGGTATGTTCCATTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATG	2553
Db	62456		
		CCCTATGTGCCAATTTCACTTGTTCACAGGCAGGAAGTTGGGGAACCTTCAGGGAGATG	62515
Qy	2554	GGGTCTTGGGGTAAAGGGGGATGTCTACTCATGTTCAGGGAATTGGGGGTTGAGGAAGCA	2613
Db	62516		
		AGGTTTTGGAGTAAAGGGGCAATGTTTGCTCATCTCAGGGGGTTGGGGGTTGAGGAAGGG	62575
Qy	2614	CAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCCA	2673
Db	62576		
		CAGGCCCTGTCAGGAGCAAACATGAGTACCCACAGGAGGCCATCAGAACCCTCACCCCA	62635
Qy	2674	GAACCAAAGGGGTCAGCCCTGGACACCTCACCCAG-----GATGTGGCTTCTTTTTC	2725
Db	62636		
		GAACCAAAGGGGTCAGCCCTGGGCACCCACACAGGGGTGACAGGATGTGGCTCCTTCTC	62695
Qy	2726	ACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCTCATCTCAGAGGGTGACTCAGGTCA	2785
Db	62696		
		ATTTCTGATTCCAGATCTCAGTGAGGTGAGGACCTTGTTCCTCAGAGGGTGACTCAGGTCA	62755
Qy	2786	ACGTAGGGACCCCATCTGGTCTAAAGACAGAGCGGTCCAGGATCTGCCATGCGTTTCGG	2845
Db	62756		
		CCACAGGGACCCCATCTGGTCTACAGACACAGTGGTCCAGGATCTGCCAAGAGTCCTG	62815
Qy	2846	GTGAGGAACATGAGGGAGGACTGAGGGTACCCAGGACCAGAACACTGAGGGAGACTGCA	2905
Db	62816		
		GTGAGGAATGTGAGGGAGGATTGAGGGTACCACAGGGCCAGAACGCAGATGATGACCCCA	62875
Qy	2906	CAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAGAGCATGGGCTGGGCCGTCTGCCGAG	2965
Db	62876		
		CAGAAATCAGCCCTGCTCCTGTTGTCACCCAGAGAGCATGGGCTTGGCTTCTGCTGAG	62935
Qy	2966	GTCCTTCCGTTATCCTGGGATCATTGATGTCAGGGACGGGAGGCCCTGGTCTGAGAAGG	3025
Db	62936		
		GTCCCTCTCTTATCCTGGGATCACTGGTGTACGGAGTGGGAGGCCCTGGTCTGAGGGGG	62995
Qy	3026	CTGCGCTCAGGTCACTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCA	3085
Db	62996		
		CTGCACCCAGGTCACTAGAGGGAGGGTCCCAGGCTCTGCCAGGAGTTGAGGTGAGGACCA	63055
Qy	3086	AGCGGGCACCTCACCCAGGACACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCT	3145

Db	63056	AGCAGGCTCCGCATCCAGGACACATGGGTTCCAATGAATTTTCGACATCTTTTGCTGTCGT	63115
Qy	3146	TC-CCCAAGGACCTAGGCACGTGTGGCCAGATGTTTGTCCCTCCTGTCTTCCATTCCCT	3204
Db	63116	TCTTCGGAAGACCTAGGCACAGGTGGCCAGATGTGGGGTTTCTTAGGTCCT---GTTCCC	63172
Qy	3205	TATCATGGATGTGAACTCTTGATTGGATTTCCTCAGACCAGCAAAAGGGCAGGATCCAGG	3264
Db	63173	TCTCAGGCATGTGAGCTCTTGATCTGAGTTTCTCAGGCCAGCAAAAGAGTGGGATCCAGG	63232
Qy	3265	CCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGA	3324
Db	63233	CCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCCACTCCATGA	63292
Qy	3325	GAGTGGGGATGTTCACAGAGTCCAGCCACCTCCTGGTAGCACTGAGAAGCCAGGGCTGT	3384
Db	63293	GAGTGGGGACCTCACAGAGTCCAGCCTACCTCCTTGATGGCACTGAGGGACCGGGGCTGT	63352
Qy	3385	GCTTGCGGTCTGCACCTGAGGGCCCGTGGATTCTCTCTCTGGAGCTCCAGGAACCAGG	3444
Db	63353	GCTTACAGTCTGCACCTAAGGGCCCATGGATTCTCTCTCTAGGAGCTCCAGGAACAAGG	63412
Qy	3445	CAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTG	3504
Db	63413	CAGTGAGGCCTTGGTCTGAGACAGTGTCTCTCAGGTTACAGAGCAGAGGATGCACAGGCTG	63472
Qy	3505	TGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACA	3564
Db	63473	TGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAAGACACA	63532
Qy	3565	TAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTGAGTCTGTAGAATCGACCTCTG	3624
Db	63533	TAGGACTCCAAAGAGTCTGGCCTCACCTCCCTACCATCAATCTGCGAGAATCGACCTCTG	63592
Qy	3625	CTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTTCAGGTTTTTCAGGGGACAGG	3683
Db	63593	CTGGCCGGCTATACCCTGAGGTGCTCTCTCACTTCCTCCTTCAGGTTCTGAGCAGACAGG	63652
Qy	3684	CCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA	3743
Db	63653	CCAACCG-GAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA	63711
Qy	3744	AGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCC	3803
Db	63712	AGTAAGCCTTTGTTAGAGCTCTAAGATTTGGTTCTCAGCTGAGGTCTCTCACATGCTCC	63771
Qy	3804	CTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTG	3863
Db	63772	CTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCCAGCTTTTGCCTGCACCTCTGCCTGCTG	63831
Qy	3864	CCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAG	3923
Db	63832	CCCTGACGAGAGTCATCATGTCTCTTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAG	63891
Qy	3924	CCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCAC-----	3975
Db	63892	GCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGGTGGGTGCACAGGCTCCTACTACTGAGG	63951
Qy	3976	-----CTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGC	4019

Db	63952	AGCAGGAGGCTGCTGTCTCCTCCTCCTCCTCCTGGTCCCTGGCACCTGGAGGAAGTGC	64011
Qy	4020	CCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCCTTCCCCTA	4079
Db	64012	CTGCTGCTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCCCTA	64071
Qy	4080	CCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTGAAGAGGAGG	4139
Db	64072	CCATCAGCTTCACTTGTCTGGAGGCAACCCAATGAGGGTTCAGCAGCCAAGAAGAGGAGG	64131
Qy	4140	GGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGG	4199
Db	64132	GGCCAAGCACCTCGCCTGACGCAGAGTCCTTGTTCGAGAAGCACTCAGTAACAAGGTGG	64191
Qy	4200	CTGATTTGGTTGGTTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAG	4259
Db	64192	ATGAGTTGGCTCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAG	64251
Qy	4260	AAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAG	4319
Db	64252	AAATGCTGGAGAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAG	64311
Qy	4320	CCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCC	4379
Db	64312	CCTCCGAGTCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCGCCAGCA	64371
Qy	4380	ACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATC	4439
Db	64372	ACACCTACACCCTTGTCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAATC	64431
Qy	4440	AGATCATGCCCAAGACAGGCTTCTTGATAATTGTCTGGTTCATGATTGCAATGGAGGGCG	4499
Db	64432	AGATCTTTCCCAAGACAGGCTTCTTGATAATCGTCTGGGCACAATTGCAATGGAGGGCG	64491
Qy	4500	GCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGA	4559
Db	64492	ACAGCGCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGA	64551
Qy	4560	GGGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAA	4619
Db	64552	GGGAGCACACTGTCTATGGGGAGCCAGGAAGTGTCTACCCAAGATTGGGTGCAGGAAA	64611
Qy	4620	AGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGG	4678
Db	64612	ACTACCTGGAGTACCGGCAGGTACCGGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGG	64671
Qy	4679	GTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCA	4738
Db	64672	GTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCA	64731
Qy	4739	GTGCAAGAGTTCGCTTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAG	4798
Db	64732	ATGCAAGAGTTCGCATTGCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAG	64791
Qy	4799	AGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG----GGACTGGGCCAGTG	4854
Db	64792	AGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCTGGGCCAGTG	64851
Qy	4855	CACCTTCCAGGGCCGCTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTT	4914
Db	64852	CATCTAACA--GCCCTGTGCAGCAGCTTCCCCTGCCTCGTGTAAACATGAGGCCCATTCCTT	64909

```

Qy      4915 CACTC-----TGAAGAGAGCGGTCAGTGTTCAGTAGTAGGTTCTGTTCTATTGGGTGA 4970
        |||||      ||||| |  ||||| ||||| ||||| || ||||| |||
Db      64910 CACTCTGTTTGAAGAAAATAGTCAGTGTTCCTTAGTAGTGGGTTCTATTTTGTGGATGA 64969

Qy      4971 CTTGGAGATTATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGG 5030
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      64970 CTTGGAGATTATCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTTAATGGATGG 65028

Qy      5031 TTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATAT 5090
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65029 TTGAATTAACCTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATAT 65088

Qy      5091 AGTTTAAGGGTAAGAGTCTTGTGTTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAA 5150
        ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65089 AGTTTAGGAGTAAGAGTCTTGTTTTTTTATTTCAGATTGGGAAATCCGTTCTATTTTGTGAA 65148

Qy      5151 TTGGG---ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAA 5207
        || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65149 TTTGGGACATAATAACAGCAGTGGAGTAAGTATTTAGAAAGTGTG---AATTCACCGTGAA 65205

Qy      5208 ATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAG 5267
        |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65206 ATAGGTGAGAT-----AAATTAAAGATACTTAATTCCCGCCTTATGCCTCAG 65253

Qy      5268 TCTATTCTGTAAAATTT-TTAAAGATATATGCATACCTGGATTTCCTTGCTTCTTTGAG 5326
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65254 TCTATTCTGTAAAATTTAAAAAATATATATGCATACCTGGATTTCCTTGCTTC---GTG 65310

Qy      5327 AATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCT 5386
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65311 AATGTAAGAGAAATTAAATCTGAATAAATAATTCTTCTGTAACTGGCTCATTTCTTCT 65370

Qy      5387 CCATGCACCTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTA 5446
        | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65371 CTATGCACCTGAGCATCTGCTCTGTGGAAGGCCCAGGATTAGTAGTGGAGATACTAGGGTA 65430

Qy      5447 AGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGA 5506
        ||||| || |||| ||||| ||||| || |||| ||||| |||||
Db      65431 AGCCAGACACACACCTACCGATAGGGTATTAAGAGTCTAGGAGCGGGTCATATAATTAA 65490

Qy      5507 GGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGGTGTGGGGC 5566
        |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65491 GGTGACAAGATGTCCTCTAAGATGTAGGGGAAAAGT----AACGAGTGTGGGTATGGGGC 65546

Qy      5567 TCCGGGTGAGAGTGGTGGAGTGTCATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAA 5626
        ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      65547 TCCAGGTGAGAGTGGTCGGGTGTAAATTCCTGTG-TGGGGCCTTTGGGCTTTGGGAAA 65605

Qy      5627 CTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        || || || ||||| ||||| ||||| ||||| ||||| |||||
Db      65606 CTCCATTTTCTTCTGAGGGATCTGATTCTAATGAAGCTTGGTGGGTCC 65653

```

Search completed: August 25, 2006, 18:36:48
Job time : 30927 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e- 8.rng.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-8.rng.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 08:55:59 ; Search time 3165 Seconds
(without alignments)
12499.380 Million cell updates/sec

Title: US-08-819-669E-8
Perfect score: 5674
Sequence: 1 CCCGGGGCACCCTGGCATC.....TAATGATCTTGGGTGGATCC 5674

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	5674	100.0	5674	2	AAQ72477	Aaq72477 Tumour re
2	5674	100.0	5674	2	AAX84113	Aax84113 MAGE-1 ge
3	5672.4	99.9	5674	2	AAQ32352	Aaq32352 MAGE-1 nu
4	5650.8	99.6	5724	2	AAQ98902	Aaq98902 Tumour re
5	2655	46.8	11495	2	ABQ76203	Abq76203 Human tum
6	2513.6	44.3	4895	2	ABQ76204	Abq76204 Human tum
7	2513.6	44.3	4895	7	ADS73099	Ads73099 Human kid
8	2513.6	44.3	4895	7	ADW41953	Adw41953 cDNA elev
9	2429.6	42.8	4736	2	ABQ76206	Abq76206 Human tum
10	2422.8	42.7	4741	2	ABQ76205	Abq76205 Human tum
11	2419	42.6	2419	2	AAQ32351	Aaq32351 Antigen E
12	2419	42.6	2419	2	AAQ72476	Aaq72476 Tumour re
13	2419	42.6	2419	2	AAX84112	Aax84112 Antigen E
14	2415.8	42.6	2419	2	AAT05086	Aat05086 MZ2-MEL a
15	2408	42.4	2420	2	AAQ72472	Aaq72472 Tumour re
16	2408	42.4	2420	2	AAQ85435	Aaq85435 Human mel
17	2408	42.4	2420	2	ABQ76198	Abq76198 Human tum
18	2408	42.4	2420	8	ABQ83847	Abq83847 Human MAG
19	2408	42.4	2420	10	ADC09583	Adc09583 MAGE-1 DN
20	2408	42.4	2420	12	ADM72822	Adm72822 Human MAG
21	2408	42.4	2420	12	ADQ36554	Adq36554 Human MAG
22	2408	42.4	2420	13	ADT93875	Adt93875 Non-small
23	2408	42.4	2420	14	ADW44360	Adw44360 Human mel
24	2408	42.4	2420	15	AEF02866	Aef02866 Wild-type
25	2408	42.4	2420	15	AEF13905	Aef13905 Human MAG
26	2404.8	42.4	2420	9	ACD42236	Acd42236 Human MAG
27	2404.8	42.4	2420	9	ACH04045	Ach04045 Human cDN
28	2400.6	42.3	2418	2	AAX84103	Aax84103 E antigen
c 29	2307.6	40.7	302250	6	ABL67703	Abl67703 Oesophagu
30	2306	40.6	302250	6	ABL67703	Abl67703 Oesophagu
31	2117.8	37.3	4559	2	ABQ76199	Abq76199 Human tum
32	2117.8	37.3	4559	8	ABQ83848	Abq83848 Human MAG
33	2117.8	37.3	4559	10	ADC09584	Adc09584 MAGE-2 DN
34	2117.8	37.3	4559	12	ADM72823	Adm72823 Human MAG
35	2058.8	36.3	4157	2	AAQ72478	Aaq72478 Tumour re
36	2058.8	36.3	4157	2	AAX84114	Aax84114 MAGE-2 ge
37	2057.2	36.3	4157	2	AAQ32353	Aaq32353 MAGE-2 ge
38	1945	34.3	4523	4	AAD06131	Aad06131 Human MAG
39	1945	34.3	4523	12	ADO23388	Ado23388 DNA encod
40	1932	34.1	2014	8	ABX95024	Abx95024 DNA encod
41	1765.8	31.1	4204	4	AAS02056	Aas02056 DNA encod
42	1765.8	31.1	4204	9	ACH04024	Ach04024 Human cDN
43	1762.6	31.1	4204	2	ABQ76200	Abq76200 Human tum
44	1762.6	31.1	4204	2	AAX26974	Aax26974 cDNA enco
45	1762.6	31.1	4204	3	AAA37927	Aaa37927 Human MAG

ALIGNMENTS

RESULT 1
AAQ72477

ID AAQ72477 standard; DNA; 5674 BP.
XX
AC AAQ72477;
XX
DT 25-MAR-2003 (revised)
DT 22-JUN-1995 (first entry)
XX
DE Tumour rejection antigen MAGE-1 encoding DNA.
XX
KW Tumour rejection antigen; melanoma antigen-1; MAGE-1; MAGE-3; cancer;
KW cytolytic T cells; antigen D; human leucocyte antigen; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 3881..4711
FT /*tag= a
XX
PN WO9423031-A1.
XX
PD 13-OCT-1994.
XX
PF 17-MAR-1994; 94WO-US002877.
XX
PR 26-MAR-1993; 93US-00037230.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Gaugler B, Van Den Eynde B, Boon-Falleur T, Van Der Bruggen P;
XX
DR WPI; 1994-333192/41.
XX
PT New tumour rejection antigen precursor MAGE3 - useful in treatment and
PT diagnosis of cancer.
XX
PS Example 26; Page 59; 105pp; English.
XX
CC AAQ72477 is the DNA sequence which encodes melanoma antigen-1 (MAGE-1).
CC Another melanoma antigen MAGE-3 is encoded by AAQ72470, this is a tumour
CC rejection antigen precursor. Melanomas characterised by the expression of
CC MAGE-3 can be detected, or monitored, by contacting a test sample with an
CC agent that can recognise MAGE-3. The melanoma can be treated by the
CC administration of cytolytic T cells specific for the complex of antigen D
CC (the mature rejection antigen derived from MAGE-3) and a human leucocyte
CC antigen (esp. HLA-A1). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 U; 0 Other;

Query Match 100.0%; Score 5674; DB 2; Length 5674;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
|||||
Db 1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy 61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
|||||
Db 61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy 121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Db	121		CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Qy	181		TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Db	181		TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241		CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241		CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301		AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301		AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361		TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361		TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421		CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421		CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601		CCCCACATCCCCACCCCATCCCTCAACCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601		CCCCACATCCCCACCCCATCCCTCAACCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661		CACCCCCACCCCAACCCCAACCCCAACCCCAACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Db	661		CACCCCCACCCCAACCCCAACCCCAACCCCAACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Qy	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATGTGTTGGGGCAGAGA	780
Db	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATGTGTTGGGGCAGAGA	780
Qy	781		GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781		GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901		GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901		GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961		CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961		CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021		TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080

Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTTGGCAGAATCC	1380
Db	1321	CCCACCCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980

Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGATACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGATACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880

Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTTGCTGTACCCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTTGCTGTACCCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCTCTCTGTCCTTCCATTCTTATCATGGATGTGAACCTTTGATTGGATTCTCTCAG	3240
Db	3181	GTCCCTCTCTGTCCTTCCATTCTTATCATGGATGTGAACCTTTGATTGGATTCTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCT	3840

Db	3781		AGCTGAGGCCCTCTCACACACTCCCTCTCTCCCCAGGCCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961		TGTGCAGGCTGCCACCTCCTCCTCCTCCTCTGGTCTGGGCACCTTGAGGAGGTGCC	4020
Db	3961		TGTGCAGGCTGCCACCTCCTCCTCCTCCTCTGGTCTGGGCACCTTGAGGAGGTGCC	4020
Qy	4021		CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021		CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141		GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141		GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201		TGATTTGGTTGGTTTCTGCTCCTCAAATATCGAGCCAGGAGCCAGTCACAAAGGCAGA	4260
Db	4201		TGATTTGGTTGGTTTCTGCTCCTCAAATATCGAGCCAGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261		AATGCTGGAGAGTGTACATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261		AATGCTGGAGAGTGTACATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321		CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321		CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381		CTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381		CTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501		CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501		CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561		GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561		GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621		GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621		GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681		CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740

Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAATAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAATAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACCTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACCTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCCTTCT	5640

Qy 5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
 |||
 Db 5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

RESULT 2

AAX84113

ID AAX84113 standard; DNA; 5674 BP.

XX

AC AAX84113;

XX

DT 08-SEP-1999 (first entry)

XX

DE MAGE-1 gene.

XX

KW Tumour rejection antigen; vaccine; cancer; MAGE-1 gene; ss.

XX

OS Homo sapiens.

XX

PN US5925729-A.

XX

PD 20-JUL-1999.

XX

PF 02-MAY-1994; 94US-00142368.

XX

PR 23-MAY-1991; 91US-00705702.

PR 09-JUL-1991; 91US-00728838.

PR 23-SEP-1991; 91US-00764365.

PR 12-DEC-1991; 91US-00807043.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Van Der Bruggen P, Traversari C, Lurquin C, Boon T, De Plaen E;

PI Van Pel A, Chomez P, Van Den Eynde B;

XX

DR WPI; 1999-418294/35.

XX

PT New tumour rejection antigen is useful as a vaccine against cancerous diseases.

XX

PS Disclosure; Col 39-46; 58pp; English.

XX

CC This sequence represents the MAGE-1 gene sequence. The invention relates

CC to a tumour rejection antigen sequence that is useful as a tumour

CC rejection antigen for vaccination against cancerous conditions

XX

SQ Sequence 5674 BP; 1276 A; 1644 C; 1569 G; 1185 T; 0 U; 0 Other;

Query Match 100.0%; Score 5674; DB 2; Length 5674;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5674; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
 |||
 Db 1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy 61 ATCCAAACATCTTCACGCTCAGCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
 |||
 Db 61 ATCCAAACATCTTCACGCTCAGCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy	121	CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Db	121	CTCTCAACCCAGGGAAGCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Qy	181	TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Db	181	TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241	CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301	AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361	TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421	CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481	CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCATCCGCCAGCCATTCCACCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCATCCGCCAGCCATTCCACCCT	660
Qy	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCCACCCCCACGCCACTCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080

Db	1021		TTCTCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081		GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141		CCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201		CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201		CCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261		ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321		CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321		CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381		GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381		GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441		TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441		TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501		ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501		ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561		ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561		ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621		CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621		CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681		CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681		CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741		GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCAGGCATTAGGGTCAGG	1800
Db	1741		GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCAGGCATTAGGGTCAGG	1800
Qy	1801		ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801		ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861		CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861		CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921		TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980

Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTGAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGA CT CAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880

Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGATTCTT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGATTCTT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCTGAGTACCTCTCACTTCCT	3660
Qy	3661	CCTTCAGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGTTTTTCAGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721	GAGCACCAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780

Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCTTGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCTTGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCACTAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCACTAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740

Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGAATGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAATAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAATAAGAAATTAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATA	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATA	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCTTCT	5640

```

Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
        ||||||||||||||||||||||||||||||||||||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 3

AAQ32352

ID AAQ32352 standard; DNA; 5674 BP.

XX

AC AAQ32352;

XX

DT 25-MAR-2003 (revised)

DT 22-APR-1993 (first entry)

XX

DE MAGE-1 nucleic acid.

XX

KW melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;

KW tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 3881..4711

FT /*tag= a

XX

PN WO9220356-A1.

XX

PD 26-NOV-1992.

XX

PF 22-MAY-1992; 92WO-US004354.

XX

PR 23-MAY-1991; 91US-00705702.

PR 09-JUL-1991; 91US-00728838.

PR 23-SEP-1991; 91US-00764364.

PR 12-DEC-1991; 91US-00807043.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Boon T, Van Der Bruggen P, Van Den Eynde B, Van Pel A, De Plaen E;

PI Lurquin C, Chomez P, Traversari C;

XX

DR WPI; 1992-415460/50.

XX

PT Nucleic acid mol. encoding a human tumour rejection antigen precursor -

PT useful as an immunostimulant in a vaccine for treating and preventing

PT cancers, also useful in diagnosis.

XX

PS Disclosure; Page 71-73; 142pp; English.

XX

CC The sequences given in AAQ32352-69 represent a new family of genes
 CC referred to as melanoma antigens (MAGE). The cDNAs of this gene family
 CC were identified during the isolation of the antigen E gene. The MAGE
 CC cDNAs, when tested, did not transfer expression of antigen E, but they
 CC did show substantial homology to the antigen E cDNA sequence. The MAGE
 CC DNAs share a certain degree of homology with each other and are expressed
 CC in tumour cells including several types of human tumor cells as well as
 CC in human tumors. MAGE expression is not restricted to melanomas. MAGE
 CC refers to a family of tumor rejection antigen precursors. The antigens
 CC resulting from these genes are referred to as MAGE TRAs or melanoma

CC antigen tumor rejection antigens. See also AAQ32351. (Updated on 25-MAR-
CC 2003 to correct PN field.)

XX

SQ Sequence 5674 BP; 1277 A; 1644 C; 1568 G; 1185 T; 0 U; 0 Other;

Query Match 99.9%; Score 5672.4; DB 2; Length 5674;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5673; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db     61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

Qy    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db    121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db    181 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300
      |||
Db    241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360
      |||
Db    301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420
      |||
Db    361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480
      |||
Db    421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Qy    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540
      |||
Db    481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Qy    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCTATCCAACCCCCA 600
      |||
Db    541 CCCCCTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCTATCCAACCCCCA 600

Qy    601 CCCCACATCCCCCACCCTCAACCCCTGATGCCCATCCGCCAGCCATTCCACCCT 660
      |||
Db    601 CCCCACATCCCCCACCCTCAACCCCTGATGCCCATCCGCCAGCCATTCCACCCT 660

Qy    661 CACCCCCACCCCCACCCCCACGCCCCTCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720
      |||
Db    661 CACCCCCACCCCCACCCCCACGCCCCTCCACCCCCACCCAGGCAGGATCCGGTTCCCG 720

Qy    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTTGTGGGGCAGAGA 780
      |||
Db    721 CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTTGTGGGGCAGAGA 780
```

Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740

Db	1681		1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCAGGATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCAGGATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTCAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACCTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGTCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640

Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGATTCTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGAATTCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGAATTCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540

Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTAC	4080
Qy	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTATCAAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440

Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAACTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400

```

Db      5341  |||||TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA 5400
Qy      5401  TCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Db      5401  |||||TCTGCTTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC 5460
Qy      5461  CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Db      5461  |||||CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC 5520
Qy      5521  CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Db      5521  |||||CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG 5580
Qy      5581  GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
Db      5581  |||||GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT 5640
Qy      5641  GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
Db      5641  |||||GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 4

AAQ98902

ID AAQ98902 standard; DNA; 5724 BP.

XX

AC AAQ98902;

XX

DT 28-FEB-1996 (first entry)

XX

DE Tumour rejection antigen (MAGE-1) gene.

XX

KW Tumour rejection antigen; MAGE-1; monoclonal antibody; MAb; diagnosis;

KW immunoassay; cancer; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 3881..4711

FT /*tag= a

FT /product= "Tumour rejection antigen MAGE-1."

FT /note= "The CDS is not indicated in the text of the
FT specification but is suggested in the layout of the
FT sequence."

XX

PN WO9520974-A1.

XX

PD 10-AUG-1995.

XX

PF 05-JAN-1995; 95WO-US000095.

XX

PR 01-FEB-1994; 94US-00190411.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

PA (SLOK) MEMORIAL SLOAN-KETTERING CANCER CENT.

XX

PI Chen Y, Stockert E, Chen Y, Garin-Chesa P, Rettig WJ;

PI Van Der Bruggen P, Boon-Falleur T, Old LJ;

XX

XX

XX

XX

XX

SQ Sequence 5724 BP; 1282 A; 1653 C; 1589 G; 1200 T; 0 U; 0 Other;

Query Match 99.6%; Score 5650.8; DB 2; Length 5724;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5652; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCGGGGCACCACCTGGCATCCCTCCCCCTACCACCCCCAATCCCTCCCTTTACGCCACCC 60

Db 1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy 61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCTG 120
 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 61 ATCAAACATCTTCACGCTACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCACCCCTG 120

Qy 121 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
 |||||

Db 121 CTCTCAACCCAGGGAAGCCCAGGTGCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180

Qy 181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Db 181 TTAGAGAGAAGCGAGGTTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240

Qy 241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Db 241 CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC 300

Qy 301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCTGGACCATCTGGTGGTGGACTTC 360
 |||
 |

Db 301 AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC 360

Qy 361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Db 361 TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG 420

Qy 421 CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT 480

Db 421 CTC CGT GTG ATC AGG GAAG GGCT GCT TAGG AGAG GGC AGC GTCC AGG CTCT GCC AGAC AT 480

Qy 481 CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC 540

Db 481 CATGCTCAGGATTCTCAAGGAGGGGCTGAGGGTCCCTAAGACCCGACTCCCGTGACCCAAC 540

Qy 541 CCCCAC TCCAAT GCTCA CTCCCG TGACCA ACCCC CTTCAT TGTCAT TCCAAC CCCCCA 600

Db	541	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCAATTCCAACCCCCA	600
Qy	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Db	601	CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCT	660
Qy	661	CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Db	661	CACCCCCACCCCAACCCCAACGCCCCACTCCACCCCAACCCAGGCAGGATCCGGTTCCCG	720
Qy	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721	CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781	GAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841	CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Db	901	GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAGA	960
Qy	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACCTCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACCTCAATCCCCACTCCCACCCATTTCGCATTCCCATTCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCTTCTGCCACCTCACCTCACTGCCCCAAC	1320
Qy	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Db	1321	CCCACCTCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCATTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCCGTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCCGTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGGGCGGCTTGAG	1500

Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCCTACCCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCCTCAGAGGACCCAGCACCCCTAGGACACCGCACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400

Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAGGGGTCAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Qy	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACCTTGATTTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360

Db	3301	CAGAGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCAGGTCTGCACCCTGAGGGCCGTGGATTCTCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCAGGTCTGCACCCTGAGGGCCGTGGATTCTCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCTCT	3660
Db	3601	TCAGTCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCTCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Db	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780
Qy	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781	AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841	CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901	TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGCTTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Db	3961	TGTGCAGGCTGCCACCTCCTCCTCTCTCTGCTTGGTCTGGGCACCCTGGAGGAGGTGCC	4020
Qy	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTCCCCTACTAC	4080
Db	4021	CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTCCCCTACTAC	4080
Qy	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081	CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141	GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260

Db	4201	TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Db	4261	AATGCTGGAGAGTGTCAATCAAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGC	4320
Qy	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321	CTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381	CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441	GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501	CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561	GGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAAT	5160

Qy	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTG	5580
Qy	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640
Db	5581	GTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCT	5640
Qy	5641	GGGGGAGCTGATTG	5654
Db	5641	GGGGGAGCTGGCTG	5654

RESULT 5

ABQ76203

ID ABQ76203 standard; DNA; 11495 BP.

XX

AC ABQ76203;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human tumour antigen MAGE-4a DNA.

XX

KW Tumour antigen; human; vaccine; cellular immune response; immunogen;
cancer; tumour; MAGE-4a; ds.

XX

OS Homo sapiens.

XX

PN US6287569-B1.

XX

PD 11-SEP-2001.

XX

PF 06-APR-1998; 98US-00056105.

XX

PR 10-APR-1997; 97US-0043467P.

XX

PA (REGC) UNIV CALIFORNIA.
XX
PI Kipps TJ, Wu Y;
XX
DR WPI; 1998-583198/49.
XX
PT Generating cellular immune response in patient to target protein -
PT comprises introducing vector with nucleotide sequence encoding immunogen
PT comprising protein processing signal into cell of patient.
XX
PS Disclosure; Col 35-44; 6lpp; English.
XX
CC This invention describes a novel method for generating a cellular immune
CC response in a patient to a target protein or its fragment. The method
CC involves introducing a vector containing a nucleotide sequence encoding a
CC chimeric immunogen comprising a protein processing signal and the target
CC protein or its fragment. The immunogen is produced by the cells and
CC processed so that the target protein or its fragment is presented to the
CC patients immune system and a cellular immune response is initiated. The
CC method and vectors can be used as a form of vaccination and could be used
CC to generate a cellular immune response in patients to, e.g. cancerous
CC tumours. The cellular immune response is the predominant immune response
CC in the patient. This sequence represents a DNA fragment which encodes the
CC human tumour antigen MAGE-4a described in the method of the invention.
CC Note: The information in this spec has been previously disclosed in
CC WO199845444 however this spec contained no sequence information
XX
SQ Sequence 11495 BP; 2530 A; 3788 C; 2924 G; 2253 T; 0 U; 0 Other;

Query Match 46.8%; Score 2655; DB 2; Length 11495;
Best Local Similarity 73.6%; Pred. No. 0;
Matches 4231; Conservative 0; Mismatches 1100; Indels 416; Gaps 50;

Qy	21	CCTCCCCCTACCACCCCAATCCCTTTCACGCCACCCATCCAAACATCTTCACGCTC	80
Db	5969	CCAGCACCCCTATCTCCCCAAACCCCACTACCCTTATGTCCTCATCCCCACCCCAAC	6028
Qy	81	ACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTGCTCTCAACCCAGGGAAGC-C	139
Db	6029	ACCACTATCCCCATCCAGGTTGAATCGCATTCCGTTTCTGCTTTCACCCAGGGAAGCTC	6088
Qy	140	CAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGGTTAGAGAGAAGCGAGGTTT	199
Db	6089	CAGGTTCTGGATGTGATGCCAGTGACTTGTGCATTGGGGGTTAGAGAGACGCTAGCTTC	6148
Qy	200	TCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGGCCCA-GCTCTGTAAGGAGG	258
Db	6149	TCAGTCTGACAGGCAGCTTGGGATTGGCAGAGGGAAGCCGGTCCAGGCTCTGTGAGGTGG	6208
Qy	259	CAAGGTGACATGCTGAGGGAGGACT---GAGGACCCACTTACCCAGATAGAGGACCCCA	315
Db	6209	CATAGTGAGAAGCTGAGGGAGAAGTCGGGAGGCCCTCTCCACCCAGATAGACGACCCCA	6268
Qy	316	AATAATCC-----CTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTCTCAGGC	366
Db	6269	AATAATCCGGCACCCCTCCTGCTTCCAGTCCTGGGCCACCCGTGGGCGGACTTCTGAGTC	6328
Qy	367	TGGGCCACCCCAAGCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAGCTCCGT	426
Db	6329	TGGGACGCCCACCACCCCACTGCCGCTGAAGCCGCAGGGACTATGGAGTCAGAGCTTGGT	6388

Qy	427	GTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACATCATGCT	486
Db	6389	GTGATCAGTGCAGGACTGGTGGGGGT-----AGGCTCTGCCAGGCATCAACGT	6436
Qy	487	CAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCCACTCCCCTGACCCAACCCCCAC	546
Db	6437	CAGGACCCTAGGAGAGGGCTGAGTGTCCCCCA---CCCCCATTCCTATCCCCCTACCCCTT	6493
Qy	547	TCCAATGCTCACTCCCGTGACCCAACCCCCCTCTTCATTGTCTATTCCAACCCCCACCCCAC	606
Db	6494	TCCCATCTGCACTCCC-----TACCCCATCTGTACCCCC	6527
Qy	607	ATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCCTCACCCC	666
Db	6528	ATTCCCCACCTGTGCCCCCTATCTCCCCAACCCCCCAACCAGCCTCATACCCCCCTCCCC	6587
Qy	667	CACCCCCACCCCCACGCCCCACTCCCACCCCCACCCAGGCAGGATCCG-GTTCGCCGAGG	725
Db	6588	CACCCCTACCTTCATCCCCATCAGTGCAGCATCCGGTTCCACCCCTGCTTTCAATCCAGG	6647
Qy	726	AAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTTGTGGGGCAGAGAGAAGC	785
Db	6648	CAAGCCCTGGGTGGCCGGATGTGATGCCACTGACTTGTGAATTGAGGGTTAGAGAGAAGT	6707
Qy	786	GAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGGCTCTG	845
Db	6708	GAGTTTCTGGGTCTGAAGGGTGGC-TTGAATCGGCAGAGGGAAGGTGGCCAGGCTTTG	6766
Qy	846	TGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATAGAGAG	905
Db	6767	TGAAGAGGCAAGGTGAGACTCTGAGGGAGGATTCAGGAAACCCCTATCCCTGATAGAGGG	6826
Qy	906	CCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCCACCCGCGGGAAGACGTCT	965
Db	6827	TCCCAGCCCTGGACTACCC-----CGCGGAGGCTGACTTCT	6862
Qy	966	CAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTCTTCTC	1025
Db	6863	CAGACTGGGCTGCTCCCCACCTCCGCCCC-----TTCGCAACGCGTTTGTTTAAGCCAC	6917
Qy	1026	CCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGGGCAGG	1085
Db	6918	AGGGGACTCTGGAGTCAGAGGTTGGTGTGATCAGGGAAGGGCTGGTTAGGAGA-GGCATG	6976
Qy	1086	GCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCCCCAAG	1145
Db	6977	GCCCAGGCCCTGCCAGGAATCAAAGTCAGAAACC-TGAGAGGGAAGTCCGAGGTTCCCAAG	7035
Qy	1146	ACTGCACTCCAATCCCCACTCCCACCCATTTCGCTATCCCATTCCCCACCCAACCCCCAT	1205
Db	7036	ATCCTAGTCTAACCCCCACTCCCACAA-----	7062
Qy	1206	CTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCACCTGACCACCACCCCT	1265
Db	7063	-----ATCCGCTGCCATTTCGCTGCTCCATTTCCTATTCCTTGCCCT	7104
Qy	1266	CCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACTGCCCCAACCCAC	1325
Db	7105	CCACCCTACCA-----	7116
Qy	1326	CCTCATCTCTCTCATGTGCCCCACTCCCATCGCTCCCCCATTCCTGGCAGAATCCGGTTT	1385

```

                                ||||| |||
Db      7117 -----GGCAGAATCCAGTTC 7131

Qy      1386 GCC-CCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACTTGAA 1444
        || ||||| |||| ||||| ||| | | | | |
Db      7132 CCCTTCTGCTATCAATCCAGGGAACCCAGGCTTGGTGCTGGGATGTTTTT----- 7183

Qy      1445 CCTCACAGATCTGAGAGAAGCCAGGTTCAATTTAATGGTTCGAGGGGCGGCTTGAGATCC 1504
        || | | | | | | | | | | | | | | | |
Db      7184 -----TGGGGGTCAGAGAATCAAGGGCATAGTCCTGAGGGGCCAGTTGAGATCG 7232

Qy      1505 ACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGGACTG 1564
        ||||| || | | | | | | | | | | | | | | | |
Db      7233 GCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAGGCAAGGTGAGACTCTGAGGAAGGACTG 7292

Qy      1565 AGGAGGCACACACCCAGGTAGATGGCCCCAAATGATCCAGTACCACCCCTGCTGCCAG 1624
        ||||| | | | | | | | | | | | | | | | | |
Db      7293 AGGAGGCCCCACCAAGATAGA-GGAACCCAAATAATCCAGCGCAGCTCCTGCTGCCAG 7351

Qy      1625 CCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCCCACT 1684
        ||||| ||||| || ||| |||| | | | | | | | |
Db      7352 TCCTGGACCACCCGG---GGGAAGACTTCTCA---GGCTAGGCCATCCAGCTCCCACT 7404

Qy      1685 GCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTTGGTC 1744
        ||||| || | | | | | | | | | | | | | | |
Db      7405 GCCACTAAAGCTACAGGGGACTCTAGAGTCAAGAGCTTGGTGTGCCCA----- 7452

Qy      1745 AGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGGACCC 1804
        ||||| ||||| || ||| |||| | | | | | | | |
Db      7453 -----AGGCAGGGCCAGGC-----TCTGCCTGGCATCGGGGTCAGGACCT 7493

Qy      1805 TGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACCCAC 1864
        || ||||| ||||| || ||||| |||| | | | | | |
Db      7494 TGAGAGGGAAC TGAGGGCGCTACACCCCAACCCATCCGCATTC-----CAACAT 7543

Qy      1865 TCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTGTCAA 1924
        | || |||| | | | | | | | | | | | | | | | |
Db      7544 GCCCAGCCCCATCCCCAATCCGTTTTGCAGAATCCATTTTT---TCCCTGCAGTCAA 7599

Qy      1925 CCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCAGGGT 1984
        ||| |||| | | | | | | | | | | | | | | | |
Db      7600 CCCCGGAAGACCTGGGAATGGT---CAGGCACTCGGATCTTGACATCCACATCGAGGGC 7656

Qy      1985 CTGATGGAGGGAAGGGG-----CTTGAACAGGGCCTCAGGGGAGCAGAGGGAG----- 2032
        | | | | | | | | | | | | | | | | | | | | |
Db      7657 TGAAGGAGGGAGAGGGTTTGGTATCATGAGCAGAGCCTCAGGGTAGCAGAGGGAGGACCC 7716

Qy      2033 -GGCCCTACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCC-----TAGGAC 2082
        ||||| ||| ||||| ||||| ||||| ||||| || | |
Db      7717 TGGCCCTCCTGGGAGATGAGGAAGGCCTCAGGAGACCCAGCACCCAAGGCAGGGAGCCC 7776

Qy      2083 ACCGCACCCCTGTCTGAGACTGAG--GCTGCCACTTCTGGCCTCAAGAATCAGAACGATG 2140
        ||| ||||| ||||| |||| | | | | | | | | | |
Db      7777 ACCCCACCCCTGTCTGAGAATGAGGTGCCTCCTCTTTTAGCCTCAGGAATCCAAGGGATG 7836

Qy      2141 GGGACTCAGATTGCAT--GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAG 2198
        | ||||| | | | | | | | | | | | | | | | |
Db      7837 GCAACTCAGGTCAGCAGAGGGGTGGGTTCGAAGCCCTTCCAGGATCAAGGAAAGGAAGAC 7896

Qy      2199 GAGGGAGGACTCAGGGGACCTTGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTC 2258
        ||||| ||||| |||| | | | | | | | | | | | |

```

Db	7897	GAGGGAGGATTTCAGGGGGCCTTGCCATTCACAGATCAGTGGAGACCTGGGCCCTGGGAGGTC	7956
Qy	2259	CAGGGCACGGTGGCCACATATGGCCCATATTTCTGCATCTTTGAGGT----GACAGGAC	2314
Db	7957	CTGGGCAAGGTAGCCACCTGTAGCTCATACTTCTGCATCTTCGAGGTCACAGAGAGGAG	8016
Qy	2315	AGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCAT	2374
Db	8017	AGGGCTATGGTCTGAGGGGTGGTACTTCAGGTCCGCAGAGGGAGGAGTCCCAGGATCTAC	8076
Qy	2375	ATGGCCCAAGATGTGCC-CCCTTCATGAGGACTGGGGATATCCCCGGCTCAGAAAAGAAGG	2433
Db	8077	AGGACCCAAGGTGTGCCACACTTCACGAGGAATGGGGATACCTGTGGCTCAGAAAGACGG	8136
Qy	2434	GACTCCACACAGTCTGGCTGTCCCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGG	2493
Db	8137	GACCCACACAGTCTGGCTGTCCCTGTTCTTAGCTCAGGGGGGACCAGAGGAGGGATGG	8196
Qy	2494	CGGTATGTTCCATTCTCACTTGTACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATG	2553
Db	8197	CCCTATGTGCCAATTTCACTTGTTCACAGGCAGGAAGTTGGGGAACCTTCAGGGAGATG	8256
Qy	2554	GGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGTTCAGGAATTGGGGGTTGAGGAAGCA	2613
Db	8257	AGGTTTTGGAGTAAAGGGGCAATGTTTGCTCATCTCAGGGGGTGGGGGTTGAGGAAGGG	8316
Qy	2614	CAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGACAAGGCTATTGGAATCCACACCCCA	2673
Db	8317	CAGGCCCCTGTCAGGAGCAAACATGAGT-ACCCACAGGAGGCCATCAGAACCTCACCCEA	8375
Qy	2674	GAACCAAAGGGGTGACGCCCTGGACACCTCACCCAG-----GATGTGGCTTCTTTTTTC	2725
Db	8376	GAACCAAAGGGGTGACGCCCTGGGCACCCACACAGGGGTGACAGGATGTGGCTCCTTCTC	8435
Qy	2726	ACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCTCATCTCAGAGGGTGACTCAGGTCA	2785
Db	8436	ATTTCTGATTCAGATCTCAGTGAGGTGAGGACCTTGTTCCTCAGAGGGTGACTCAGGTCA	8495
Qy	2786	ACGTAGGGACCCCATCTGGTCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCGG	2845
Db	8496	CCACAGGGACCCCATCTGGTCTACAGACACAGTGGTCCCAGGATCTGCCAAGAGTCCTG	8555
Qy	2846	GTGAGGAACATGAGGGAGGACTGAGGGTACCCAGGACCAGAACACTGAGGGAGACTGCA	2905
Db	8556	GTGAGGAATGTGAGGGAGGATTGAGGGTACCACAGGGCCAGAACGCAGATGATGACCCCA	8615
Qy	2906	CAGAAATCAGCCCTGCCCCTGCTGTACCCAGAGAGCATGGGCTGGGCCGTCTGCCGAG	2965
Db	8616	CAGAAATCAGCCCTGCTCTGTTGTCACCCAGAGAGCATGGGCTTGGCTTTCTGCTGAG	8675
Qy	2966	GTCCTTCCGTTATCTTGGGATCATTGATGTACGGGACGGGGAGGCCCTTGGTCTGAGAAGG	3025
Db	8676	GTCCCTCTCTTATCTTGGGATCACTGGTGTACGGAGTGGGAGGCCCTTGGTCTGAGGGGG	8735
Qy	3026	CTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCA	3085
Db	8736	CTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGGCTCTGCCAGGAGTTGAGGTGAGGACCA	8795
Qy	3086	AGCGGGCACCTCACCCAGGACACATTAATTCCAATGAATTTTGATATCTCTTGCTGCCCT	3145
Db	8796	AGCAGGGCTCCGCATCCAGGACACATGGGGTTCCAATGAATTTTCGACATCTTTTGTGTCGT	8855

Qy	3146	TC-CCCAAGGACCTAGGCACAGTGTGGCCAGATGTTTGTCCCTCCTGTCCTTCCATTCCCT	3204
Db	8856	TCTTCGGAAGACCTAGGCACAGGTGGCCAGATGTGGGGTTTCTTAGGTCCT---GTTCCC	8912
Qy	3205	TATCATGGATGTGAACTCTTGATTGTGATTCTCAGACCAGCAAAAGGGCAGGATCCAGG	3264
Db	8913	TCTCAGGCATGTGAGCTCTTGATCTGAGTTTCTCAGGCCAGCAAAAGAGTGGGATCCAGG	8972
Qy	3265	CCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGA	3324
Db	8973	CCCTGCCTGGAGAAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCCACTCCATGA	9032
Qy	3325	GAGTGGGGATGTCACAGAGTCCAGCCACCCTCCTGGTAGCACTGAGAAGCCAGGGCTGT	3384
Db	9033	GAGTGGGGACCTCACAGAGTCCAGCCTACCCTCCTTGATGGCACTGAGGGACCGGGGCTGT	9092
Qy	3385	GCTTGCGGTCTGCACCCTGAGGGCCCGTGGAATCCTCTTCCTGGAGCTCCAGGAACCAGG	3444
Db	9093	GCTTACAGTCTGCACCCTAAGGGCCCATGGATTCTCTCCTAGGAGCTCCAGGAACAAGG	9152
Qy	3445	CAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCACAGGGTG	3504
Db	9153	CAGTGAGGCCTTGGTCTGAGACAGTGTCTCAGGTTACAGAGCAGAGGATGCACAGGCTG	9212
Qy	3505	TGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAGGACACA	3564
Db	9213	TGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAAGACACA	9272
Qy	3565	TAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTGAGTCCTGTAGAATCGACCTCTG	3624
Db	9273	TAGGACTCCAAAGAGTCTGGCCTCACCTCCCTACCATCAATCCTGCAGAATCGACCTCTG	9332
Qy	3625	CTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTTCAGGTTTTCAGGGGACAGG	3683
Db	9333	CTGGCCGGCTTATACCCTGAGGTGCTCTCTCACTTCCTCCTTCAGGTTCTGAGCAGACAGG	9392
Qy	3684	CCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA	3743
Db	9393	CCAACCG-GAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAGATCTGTA	9451
Qy	3744	AGTAGGCCTTTGTGTAGAGTCTCCAAGGTTCACTTCTCAGCTGAGGCCTCTCACACTCC	3803
Db	9452	AGTAAGCCTTTGTGTAGAGCCTCTAAGATTGGTTCTCAGCTGAGGTCTCTCACATGCTCC	9511
Qy	3804	CTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCTGCCTGCTG	3863
Db	9512	CTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCCAGCTTTTGCCTGCACCTCTTGCTGCTG	9571
Qy	3864	CCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAG	3923
Db	9572	CCCTGACCAGAGTCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAG	9631
Qy	3924	CCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCAC-----	3975
Db	9632	GCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGGTGGGTGCACAGGCTCCTACTACTGAGG	9691
Qy	3976	-----CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGC	4019
Db	9692	AGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTCTGGTCCCTGGCACCCCTGGAGGAAGTGC	9751

Qy	4020	CCATGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTA	4079
Db	9752	CTGCTGCTGAGTCAGCAGGTCTCTCCCAGAGTCCTCAGGGAGCCTCTGCCTTACCCACTA	9811
Qy	4080	CCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGG	4139
Db	9812	CCATCAGCTTCACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAGAAGAGGAGG	9871
Qy	4140	GGCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGG	4199
Db	9872	GGCCAAGCACCTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTAACAAGGTGG	9931
Qy	4200	CTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAG	4259
Db	9932	ATGAGTTGGCTCATTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCACAAAGGCAG	9991
Qy	4260	AAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAG	4319
Db	9992	AAATGCTGGAGAGAGTCATCAAAAATTACAAGCGCTGCTTTCCTGTGATCTTCGGCAAAG	10051
Qy	4320	CCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCC	4379
Db	10052	CCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACCCCGCCAGCA	10111
Qy	4380	ACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATC	4439
Db	10112	ACACCTACACCTTGTCACCTGCCTGGGCCTTTCCTATGATGGCCTGCTGGGTAATAATC	10171
Qy	4440	AGATCATGCCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCG	4499
Db	10172	AGATCTTTCCCAAGACAGGCTTCCTGATAATCGTCCTGGGCACAATTGCAATGGAGGGCG	10231
Qy	4500	GCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGA	4559
Db	10232	ACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGTATGATGGGA	10291
Qy	4560	GGGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAA	4619
Db	10292	GGGAGCACACTGTCTATGGGGAGCCCAGGAACTGCTCACCCAAGATTGGGTGCAGGAAA	10351
Qy	4620	AGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGG	4678
Db	10352	ACTACCTGGAGTACCGGCAGGTACCCGGCAGTAATCCTGCGCGCTATGAGTTCCTGTGGG	10411
Qy	4679	GTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCA	4738
Db	10412	GTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGGTCAGGGTCA	10471
Qy	4739	GTGCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAG	4798
Db	10472	ATGCAAGAGTTCGCATTGCCTACCCATCCCTGCGTGAAGCAGCTTTGTTAGAGGAGGAAG	10531
Qy	4799	AGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG---GGACTGGGCCAGTG	4854
Db	10532	AGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCTGGGCCAGTG	10591
Qy	4855	CACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATCTT	4914
Db	10592	CATCTAACA--GCCCTGTGCAGCAGCTTCCCTTGCCCTCGTGTAAACATGAGGCCCATCTT	10649
Qy	4915	CACCTC---TGAAGAGAGCGGTCACTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGA	4970

Db	10650	CACTCTGTTTGAAGAAAATAGTCAGTGTTCCTTAGTAGTGGGTTTCTATTTTGTGGATGA	10709
Qy	4971	CTTGGAGATTTATCTTTGTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGG	5030
Db	10710	CTTGGAGATTTATCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTTAATGGATGG	10768
Qy	5031	TTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATAT	5090
Db	10769	TTGAATTAAC TTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGCTGTTAATAT	10828
Qy	5091	AGTTTAAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAA	5150
Db	10829	AGTTTAGGAGTAAGAGTCTTGTGTTTTTTATTTCAGATTGGGAAATCCGTTCTATTTTGTGAA	10888
Qy	5151	TTGGG---ATAATAACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAA	5207
Db	10889	TTTGGGACATAATAACAGCAGTGAGTAAGTATTTAGAAAGTGTG---AATTCACCGTGAA	10945
Qy	5208	ATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAG	5267
Db	10946	ATAGGTGAGAT-----AAATTAAAAGATACTTAATCCCGCCTTATGCCTCAG	10993
Qy	5268	TCTATTCTGTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCCTTCTTTGAGA	5327
Db	10994	TCTATTCTGTAAAATTTAAAAATATATATGCATACCTGGATTTCCTTGGCCTC---GTGA	11050
Qy	5328	ATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTC	5387
Db	11051	ATGTAAGAGAAATTAATCTGAATAAATAATTCTTTCTGTAACTGGCTCATTTCTTCTC	11110
Qy	5388	CATGCACTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAA	5447
Db	11111	TATGCACTGAGCATCTGCTCTGTGGAAGGCCCAGGATTAGTAGTGGAGATACTAGGGTAA	11170
Qy	5448	GCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAG	5507
Db	11171	GCCAGACACACACCTACCGATAGGGTATTAAGAGTCTAGGAGCGCGGTCATATAATTAAG	11230
Qy	5508	GTGGCAAGATGTCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCT	5567
Db	11231	GTGACAAGATGTCTCTAAGATGTAGGGGAAAAGT----AACGAGTGTGGGTATGGGGCT	11286
Qy	5568	CCGGGTGAGAGTGGTGGAGTGTCATGCCCTGAGCTGGGGCATTTTGGGCTTTGGGAAAC	5627
Db	11287	CCAGGTGAGAGTGGTCGGGTGTAAATTCCTGTG-TGGGGCCTTTTGGGCTTTGGGAAAC	11345
Qy	5628	TGCAGTTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674
Db	11346	TGCATTTTCTTCTGAGGGATCTGATTCTAATGAAGCTTGGTGGGTCC	11392

Db	782	---GGCTAGGCCATCCCAGCTCCCCTGCCACTAAAGCTACAGGGGACTCTAGAGTCA--	836
Qy	1718	GCTTATGTGACCGGGGAGGGTTGGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGC	1777
Db	837	-----AGAGCTTGGTGTGCCCAAGGCAGGGCCAGG	866
Qy	1778	ATCCGCCCCGCATTAGGGTCAGGACCCTGGGAGGGAAGTCTGAGGGTCCCCACCCACACCT	1837
Db	867	CTCTGCCTGGCATCGGGTCAGGACCTTGAGAGGGAAGTCTGAGGGCGCTACACCCCCACCC	926
Qy	1838	GTCTCCTCATCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCCAACCC	1897
Db	927	CATCCGCATTC-----CAACATGCCAGCCCCATCCCCAATCCGTTTTCAGAA	976
Qy	1898	TCATCTTGTGAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCAC	1957
Db	977	TCCATTTT---TCCCCTGCAGTCAACCCCGGGAAGACCTGGGAATGGT---CAGGCAC	1029
Qy	1958	TCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAACAG	2010
Db	1030	TCGGATCTTGACATCCACATCGAGGGCTGAAGGAGGGAGAGAGTTTGGTATCATGAGCAG	1089
Qy	2011	GGCCTCAGGGGAGCAGAGGGAG-----GGCCCTACTGCGAGATGAGGGAGGCCTCAGAG	2064
Db	1090	AGCCTCAGGGTAGCAGAGGGAGGACCCTGGCCCTCTGGGAGATGAGGAAGGCCTCAGGA	1149
Qy	2065	GACCCAGCACCC-----TAGGACACCGCACCCCTGTCTGAGACTGAG--GCTGCCA	2113
Db	1150	GACCCAGCACCCCAAGGCAGGGAGCCACCCACCCCTGTCTGAGAATGAGGTGCCTCCT	1209
Qy	2114	CTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGA--CCCAG	2171
Db	1210	CCTTTAGCCTCAGGAATCCAAGGGATGGCAACTCAGGTCAGCAGAGGGGTGGGTCCAAG	1269
Qy	2172	GCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGGAATCCAGAT	2231
Db	1270	CCCTTCCAGGATCAAGGAAAGGAAGACGAGGGAGGATTTCAGGGGGCCTTGCAATCCAGAT	1329
Qy	2232	CAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTTC	2291
Db	1330	CAGTGGAGACCTGGGCCCTGGGAGGTCTGGGCAAGGTAGCCACCTGTAGCTCATACTTC	1389
Qy	2292	CTGCATCTTTGAGGT----GACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTC	2347
Db	1390	CTGCATCTTCGAGGTCACAGAGAGGAGAGGGCTATGGTCTGAGGGGTGGTACTTCAGGTC	1449
Qy	2348	AACAGAGGGAGGAGTTCCAGGATCCATATGGCCCCAAGATGTGCC-CCCTTCATGAGGACT	2406
Db	1450	CGCAGAGGGAGGAGTCCCAGGATCTACAGGACCCAAGGTGTGCCACACTTCACGAGGAAT	1509
Qy	2407	GGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTTTTAGTA	2466
Db	1510	GGGGATACCTGTGGCTCAGAAAGACGGGACCCACAGAGTCTGGCTGTCCCTGTCTCTTA	1569
Qy	2467	GCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCA	2526
Db	1570	GCTCAGGGGGGACCAGAGGAGGGATGGCCCTATGTGCCAATTTCACTTGTTCACAGGCA	1629
Qy	2527	GGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCAT	2586
Db	1630	GGAAGTTGGGGAACCTTCAGGGAGATGAGGTTTTGGAGTAAAGGGGCAATGTTTGCTCAT	1689

Qy	2587	GTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACA	2646
Db	1690	CTCAGGGGGTTGGGGGTTGAGGAAGGGCAGGCCCTGTCAGGAGCAAACATGAGT-ACCCA	1748
Qy	2647	GACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGACACCTCACCC	2706
Db	1749	CAGGAGGCCATCAGAACCCCTACCCCAGAACCAAAGGGGTCAGCCCTGGGCACCCACAC	1808
Qy	2707	AG-----GATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGGAC	2758
Db	1809	AGGGGTGACAGGATGTGGCTCCTTCTCATTTCTGATTCCAGATCTCAGTGAGGTGAGGAC	1868
Qy	2759	CTCATTTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAG	2818
Db	1869	CTTGTTCTCAGAGGGTGACTCAGGTCAACACAGGGACCCCCATCTGGTCTACAGACACAG	1928
Qy	2819	CGGTCCCAGGATCTGCCATGCGTTGCGGTGAGGAACATGAGGGAGGACTGAGGGTACCCC	2878
Db	1929	TGGTCCCAGGATCTGCCAAGAGTCCTGGTGAGGAATGTGAGGGAGGATTGAGGGTACCAC	1988
Qy	2879	AGGACCAGAACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAG	2938
Db	1989	AGGGCCAGAACGCAGATGATGACCCACAGAAATCAGCCCTGCTCCTGTTGTCACCCAG	2048
Qy	2939	AGAGCATGGGCTGGGCCGCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAG	2998
Db	2049	AGAGCATGGGCTTGGCTTCTGCTGAGGTCCCTCTCTTATCCTGGGATCACTGGTGTAC	2108
Qy	2999	GGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGG	3058
Db	2109	GGAGGGGGAGGCCTTGGTCTGAGGGGGCTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGG	2168
Qy	3059	CCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCA	3118
Db	2169	CTCTGCCAGGAGTTGAGGTGAGGACCAAGCAGGCTCCGCATCCAGGACACATGGGTTC	2228
Qy	3119	ATGAATTTTGATATCTCTTGCTGCCCTTC-CCCAAGGACCTAGGCACGTGTGGCCAGATG	3177
Db	2229	ATGAATTTGACATCTTTTGCTGTGCTTCTTCGGAAGACCTAGGCACAGGTGGCCAGATG	2288
Qy	3178	TTTGTCCCTCCTGTCTTCCATTCTTATCATGGATGTGAACTCTTGATTGGATTCT	3237
Db	2289	TGGGGTTTCTTAGGTCCT---GTTCCCTCTCAGGCATGTGAGCTCTGATCTGAGTTTCT	2345
Qy	3238	CAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAATATAAGGGCCCTGCGTGA	3297
Db	2346	CAGGCCAGCAAAAGAGTGGGATCCAGGCCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGA	2405
Qy	3298	GAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTC	3357
Db	2406	ACACAGTGGGGATCATCCACTCCATGAGAGTGGGGACCTCACAGAGTCCAGCCTACCTC	2465
Qy	3358	CTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGATT	3417
Db	2466	TTGATGGCACTGAGGGACCGGGCTGTGCTTACAGTCTGCACCTAAGGGCCCATGGATT	2525
Qy	3418	CCTCTTCTGAGCTCCAGGAACAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAG	3477
Db	2526	CCTCTCTAGGAGCTCCAGGAACAAGGCAGTGAGGCCTTGGTCTGAGACAGTGTCTCAG	2585

Qy 3478 GTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGGCCCTGAATGCACAC 3537
 || |||||
 Db 2586 GTTACAGAGCAGAGGATGCACAGGCTGTGCCAGCAGTGAATGTTTGGCCCTGAATGCACAC 2645

Qy 3538 CAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTA 3597
 |||||
 Db 2646 CAAGGGCCCCACCTGCCACAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCTCCCTA 2705

Qy 3598 CTGTCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACT 3656
 | ||| |||||
 Db 2706 CCATCAATCTGCAGAATCGACCTCTGCTGGCCGGCTATACCCTGAGGTGCTCTCTCACT 2765

Qy 3657 TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC 3716
 |||||
 Db 2766 TCCTCCTTCAGGTTCTGAGCAGACAGGCCAA-CCGGAGGACAGGATTCCCTGGAGGCCAC 2824

Qy 3717 AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT 3776
 |||||
 Db 2825 AGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCTAAGATTGGT 2884

Qy 3777 TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC 3836
 |||||
 Db 2885 TCTCAGCTGAGGTCTCTCACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCC 2944

Qy 3837 AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA 3896
 |||||
 Db 2945 AGCTTTTGCCTGCACCTTGCCTGCTGCCCTGAGCAGAGTCATCATGTCTCTTGAGCAGA 3004

Qy 3897 GGAGTCTGCACCTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG 3956
 |||||
 Db 3005 AGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGG 3064

Qy 3957 TGTGTGTGCAGGCTGCCAC-----CTCCTCCTCCTCTCCTC 3992
 || ||| |||||
 Db 3065 TGGGTGCGCAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTC 3124

Qy 3993 TGGTCCTGGGCACCTTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCTCCCCAGAGTC 4052
 |||||
 Db 3125 TGGTCCCTGGCACCCTGGAGGAAGTGCTGCTGCTGAGTCAGCAGGTCTCCCCAGAGTC 3184

Qy 4053 CTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTG 4112
 |||||
 Db 3185 CTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTTGCTGGAGGCAACCCAATG 3244

Qy 4113 AGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGT 4172
 |||||
 Db 3245 AGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAGTCCTTGT 3304

Qy 4173 TCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATC 4232
 |||||
 Db 3305 TCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTATC 3364

Qy 4233 GAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGC 4292
 |||||
 Db 3365 GAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAGC 3424

Qy 4293 ACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTG 4352
 |||
 Db 3425 GCTGCTTTCTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTG 3484

Qy 4353 ACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCT 4412

Db	3485	ACGTGAAGGAAGTGGACCCACCAGCAACACCTACACCCTTGTCACCTGCCTGGGCCTTT	3544
Qy	4413	CCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCCTTCCTGATAATTG	4472
Db	3545	CCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCAAGACAGGCCTTCCTGATAATCG	3604
Qy	4473	TCCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGC	4532
Db	3605	TCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGC	3664
Qy	4533	TGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGC	4592
Db	3665	TGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAAAC	3724
Qy	4593	TGCTCACCCAAGATTTGGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTG	4651
Db	3725	TGCTCACCCAAGATTTGGGTGCAGGAAAAC TACCTGGAGTACCGGCAGGTACCCGGCAGTA	3784
Qy	4652	ATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGA	4711
Db	3785	ATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGA	3844
Qy	4712	AAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGC	4771
Db	3845	AAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCATCCCTGC	3904
Qy	4772	GTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCA	4831
Db	3905	GTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTG	3964
Qy	4832	GTGGGAGGG-----GGACTGGGCCAGTGCACCTTCAGGGCCGCGTCCAGCAGCTTCCCTT	4887
Db	3965	TGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCTT	4022
Qy	4888	GCCTCGTGTGACATGAGGCCCATTCCTTCACTC-----TGAAGAGAGCGGTGAGTGTCTCA	4943
Db	4023	GCCTCGTGTAAACATGAGGCCCATTCCTTCACTCTGTTTGAAGAAAATAGTCAGTGTCTTA	4082
Qy	4944	GTAGTAGGTTTCTGTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATT	5003
Db	4083	GTAGTGGGTTTCTATTTTGTGGATGACTTGGAGATTTATCTCTGTTTCCTTTTACAATT	4142
Qy	5004	GTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATG	5063
Db	4143	GTTGAAATG-TTCCTTTTAATGGATGGTTGAATTAACCTCAGCATCCAAGTTTATGAATC	4201
Qy	5064	ACAGCAGTCACACAGTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAG	5123
Db	4202	GTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTAAGAGTCTTGTTTTTATTTCAG	4261
Qy	5124	ATTGGGAAATCCATTCTATTTTGTGAATTGGG---ATAATAACAGCAGTGGAAATAAGTAC	5180
Db	4262	ATTGGGAAATCCGTTCTATTTTGTGAATTTGGGACATAATAACAGCAGTGGAGTAAGTAT	4321
Qy	5181	TTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAG	5240
Db	4322	TTAGAAGTGTG---AATTCACCGTGAATAGGTGAGAT-----AAATTAAGAG	4366
Qy	5241	ATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGCAT	5300

Db	4367	ATACTTAATTCCTCCGCTTATGCCTCAGTCTATCTGTAAAATTTAAAAATATATATGCAT	4426
Qy	5301	ACCTGGATTTCCTTGCTTCTTTGAGAAATGTAAGAGAAATTAAATCTGAATAAAGAATTC	5360
Db	4427	ACCTGGATTTCCTTGCTTCT--GTGAATGTAAGAGAAATTAAATCTGAATAAATAATTC	4483
Qy	5361	TTCCTGTTCACCTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGAAGGCCCT	5420
Db	4484	TTTCTGTTAACCTGGCTCATTTCTTCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCA	4543
Qy	5421	GGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAG	5480
Db	4544	GGATTAGTAGTGGAGATACTAGGGTAAGCCAGACACACACCTACCGATAGGGTATTAAGA	4603
Qy	5481	TCTAGGAGCTGCAGTCAAGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAA	5540
Db	4604	GTCTAGGAGCGCGGTCAATAATTAAGGTGACAAGATGTCCTCTAAGATGTAGGGGAAAA	4663
Qy	5541	GTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGA	5600
Db	4664	GT----AACGAGTGTGGGTATGGGGCTCCAGGTGAGAGTGGTCGGGTGTAAATTCCTGT	4719
Qy	5601	GCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCTTCTGGGGGAGCTGATTGTAATGA	5660
Db	4720	G-TGGGGCCTTTTGGGCTTTGGGAACTCCATTTTCTTCTGAGGGATCTGATTCTAATGA	4778
Qy	5661	TCTTGGGTGGATCC	5674
Db	4779	AGCTTGGTGGGTCC	4792

ADS73099

XX

XX

XX

XX

KW

OS

XX

XX

XX

XX

PR

PA

PI

DR

XX

PT New isolated polynucleotides and polypeptides, useful for detecting the
PT presence of, and treating cancer, particularly kidney cancer by
PT stimulating T-cells specific for a tumor protein, and stimulating immune
PT response in a patient.

XX

PS Claim 1; SEQ ID NO 1696; 78pp; English.

XX

CC The invention relates to a new isolated polynucleotide (a Human kidney
CC tumour specific cDNA) comprising any one of the 1855 sequences identified
CC in the specification (or their complements, degenerate variants,
CC sequences consisting of at least 20 contiguous residues them, sequences
CC that hybridise to them under highly stringent conditions or sequences
CC having at least 75 or 90% sequence identity to the 1855 sequences. Also
CC included are detecting/determining the presence of cancer in a patient,
CC stimulating an immune response in a patient; treating kidney cancer in a
CC patient, an isolated polypeptide encoded by one of the 1855 sequences, an
CC expression vector comprising the polynucleotide operably linked to an
CC expression control sequence, a host cell transformed/transfected with the
CC vector, an isolated antibody (or its antigen-binding fragment) that
CC specifically binds to the protein, a fusion protein comprising at least
CC one the proteins, stimulating and/or expanding T-cells specific for a
CC tumour protein, an isolated T-cell population comprising the T-cells, a
CC composition comprising a first component (such as a carrier or
CC immunostimulant) and a second component (comprising one of the
CC polynucleotides, the polypeptides, an antibody, T-cell or an antigen-
CC presenting cell that expresses the polynucleotide) and a diagnostic kit
CC comprising at least one of the oligonucleotides, or at least one antibody
CC and a detection reagent comprising a reporter group. The polynucleotides,
CC polypeptides, antibodies and antigen-presenting cells are useful for
CC detecting the presence of, and treating cancer, particularly kidney
CC cancer by stimulating and/or expanding T-cells specific for a tumour
CC protein, and stimulating immune response in a patient. The present
CC sequence is one of the Human kidney tumour specific cDNAs. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=20030109434.

XX

SQ Sequence 4895 BP; 1134 A; 1235 C; 1433 G; 1093 T; 0 U; 0 Other;

Query Match 44.3%; Score 2513.6; DB 7; Length 4895;
Best Local Similarity 79.9%; Pred. No. 0;
Matches 3415; Conservative 0; Mismatches 694; Indels 165; Gaps 32;

Qy 1478 ATGGTTCTGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAG 1537
|| || ||||| ||||| ||||| || ||||| ||
Db 607 ATAGTCCTGAGGGGCCAGTTGAGATCGGCTGAGGGGAGCGGGCCAAGCTCTGTGGCGAG 666

Qy 1538 GCAAGGTGAGATGCTGAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAA 1597
||||||| ||||| ||||| ||||| || ||||| || |||||
Db 667 GCAAGGTGAGACTCTGAGGAAGGACTGAGGAGGCCCCACCCAAGATAGA-GGAACCCAA 725

Qy 1598 ATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAG 1657
|| ||||| | ||||| ||||| ||||| || |||||
Db 726 ATAATCCAGCCCACGTCTGCTGCCAGTCTGGACCACCCGG---GGGAAGACTTCTCA- 781

Qy 1658 CTGGACCACCCCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATA 1717
| | | | | ||||| ||||| || ||||| || |||||
Db 782 ---GGCTAGGCCATCCCAGCTCCCACTGCCACTAAAGCTACAGGGGACTCTAGAGTCA-- 836

Qy 1718 GCTTATGTGACCGGGGCGAGGTTGGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGC 1777
|||| || | |||||

```

Db      837 -----AGAGCTTGGTGTGCCCCAAGGCAGGGCCAGG 866
Qy      1778 ATCCGCCCCGGCATTAGGGTCAGGACCTTGGGAGGGAAC TGAGGGTTCCCCACCCACACCT 1837
      || ||| ||||| ||||| ||| ||||| ||||| | ||||| ||||
Db      867 CTCTGCCTGGCATCGGGTCAGGACCTTGAGAGGGAAC TGAGGGCGCTACACCCCCACCC 926
Qy      1838 GTCTCCTCATCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCCAACC 1897
      | | | | | | | | | | | | | | | | | | | | | |
Db      927 CATCCGCATTC-----CAACATGCCCAGCCCCATCCCCAACTCCGTTTTCAGAA 976
Qy      1898 TCATCTTGTCAGAATCCCTGCTGTCAACCCACGGAAGCCACGGAATGGCGGCCAGGCAC 1957
      || || | | | | | | | | | | | | | | | | | | | |
Db      977 TCCATTTTT---TCCCCTGCAGTCAACCCGGAAGACCTGGGAATGGT---CAGGCAC 1029
Qy      1958 TCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAACAG 2010
      ||||| ||||| ||| ||| |||| | | | | | | | | | | | |
Db      1030 TCGGATCTTGACATCCACATCGAGGGCTGAAGGAGGGAGAGAGTTTGGTATCATGAGCAG 1089
Qy      2011 GGCCTCAGGGGAGCAGAGGGAG-----GGCCCTACTGCGAGATGAGGGAGGCCTCAGAG 2064
      ||||| ||||| ||||| ||||| ||| ||||| ||||| ||||| ||
Db      1090 AGCCTCAGGGTAGCAGAGGGAGGACCTGGCCCTCTGGGAGATGAGGAAGGCCTCAGGA 1149
Qy      2065 GACCCAGCACCC-----TAGGACACCGCACCCCTGTCTGAGACTGAG--GCTGCCA 2113
      ||||| ||||| || | ||||| ||||| ||||| ||||| || ||
Db      1150 GACCCAGCACCCCAAGGCAGGGAGCCACCCACCCCTGTCTGAGAATGAGGTGCCTCCT 1209
Qy      2114 CTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGA--CCCAG 2171
      | | | ||||| |||| | |||| | |||| | | | ||| || |||
Db      1210 CCTTTAGCCTCAGGAATCCAAGGGATGGCAACTCAGGTCAGCAGAGGGGTGGGTTCAG 1269
Qy      2172 GCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGAATCCAGAT 2231
      ||| | || | | | | ||||| ||||| ||||| ||||| ||||| ||
Db      1270 CCCTTCCAGGATCAAGGAAAGGAAGACGAGGGAGGATTCAGGGGGCCTTGCAATCCAGAT 1329
Qy      2232 CAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTTC 2291
      |||| | |||| ||||| ||||| |||| | || | |||| | | || |||| ||
Db      1330 CAGTGGAGACCTGGGCCCTGGGAGGTCTGGGCAAGGTAGCCACCTGTAGCTCATACTTC 1389
Qy      2292 CTGCATCTTTGAGGT----GACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTC 2347
      ||||| |||| | |||| | |||| | |||| | |||| | |||| | |||||
Db      1390 CTGCATCTTCGAGGTCACAGAGAGGAGAGGGCTATGGTCTGAGGGGTGGTACTTCAGGTC 1449
Qy      2348 AACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCC-CCCTTCATGAGGACT 2406
      ||||| ||||| ||||| | | | ||||| ||||| ||||| ||||| ||
Db      1450 CGCAGAGGGAGGAGTCCCAGGATCTACAGGACCAAGGTGTGCCACACTTCACGAGGAAT 1509
Qy      2407 GGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTTTTAGTA 2466
      ||||| | | ||||| ||||| |||| | |||| | ||||| ||||| || ||
Db      1510 GGGGATACCTGTGGCTCAGAAAGACGGGACCCACAGAGTCTGGCTGTCCCTGTCTCTTA 1569
Qy      2467 GCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCA 2526
      |||| | ||||| ||||| ||||| |||| | |||| | ||||| ||||| ||
Db      1570 GCTCAGGGGGGACCAGAGGAGGGATGGCCCTATGTGCCAATTCCTTGTTCACAGGCA 1629
Qy      2527 GGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGATGTCTACTCAT 2586
      ||||| |||| | ||||| |||| | |||| | |||| | |||| | |||||
Db      1630 GGAAGTTGGGGAACCTTCAGGGAGATGAGGTTTGGAGTAAAGGGGCAATGTTTGCTCAT 1689
Qy      2587 GTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACA 2646
      ||||| ||||| ||||| |||| | |||| | |||| | |||| | |||||
Db      1690 CTCAGGGGGTTGGGGGTTGAGGAAGGGCAGGCCCTGTCAGGAGCAACATGAGT-ACCCA 1748

```

[illegible]

Qy	3538	CAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTA	3597
Db	2646	CAAGGGCCCCACCTGCCACAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCTCCCTA	2705
Qy	3598	CTGTCACTCCTGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACT	3656
Db	2706	CCATCAATCCTGCAGAATCGACCTCTGCTGGCCGGCTATACCCTGAGGTGCTCTCTCACT	2765
Qy	3657	TCCTCCTTCAGGTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC	3716
Db	2766	TCCTCCTTCAGGTTCTGAGCAGACAGGCCAA-CCGGAGGACAGGATTCCCTGGAGGCCAC	2824
Qy	3717	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT	3776
Db	2825	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCTAAGATTTGGT	2884
Qy	3777	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC	3836
Db	2885	TCTCAGCTGAGGTCTCTCACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCC	2944
Qy	3837	AGCTCCTGCCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	2945	AGCTTTTGCCCTGCACCTCTGCCTGCTGCCCTGAGCAGAGTCATCATGTCTCTTGAGCAGA	3004
Qy	3897	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Db	3005	AGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGG	3064
Qy	3957	TGTGTGTGCAGGCTGCCAC-----CTCCTCCTCCTCTCCTC	3992
Db	3065	TGGGTGCGCAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTC	3124
Qy	3993	TGGTCCTGGGCACCTTGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTC	4052
Db	3125	TGGTCCCTGGCACCTTGAGGAAGTGCTGCTGCTGAGTCAGCAGGTCTCCCCAGAGTC	3184
Qy	4053	CTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTG	4112
Db	3185	CTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTTGCTGGAGGCAACCCAATG	3244
Qy	4113	AGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGATCCTGGAGTCCTTGT	4172
Db	3245	AGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAGTCCTTGT	3304
Qy	4173	TCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATC	4232
Db	3305	TCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTATC	3364
Qy	4233	GAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGC	4292
Db	3365	GAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAGC	3424
Qy	4293	ACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTG	4352
Db	3425	GCTGCTTTCTGTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTG	3484
Qy	4353	ACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCT	4412
Db	3485	ACGTGAAGGAAGTGGACCCACCGACCAACACCTACACCCTTGTACCTGCCTGGGCCTTT	3544
Qy	4413	CCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTG	4472

Db	3545	 CCTATGATGGCCTGCTGGGTAATAATCAGATCTTTCCCAAGACAGGCCTTCTGATAATCG	3604
Qy	4473	TCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGC	4532
Db	3605	 TCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGC	3664
Qy	4533	TGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGC	4592
Db	3665	 TGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAAAC	3724
Qy	4593	TGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTG	4651
Db	3725	 TGCTCACCCAAGATTTGGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTACCCGGCAGTA	3784
Qy	4652	ATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGA	4711
Db	3785	 ATCCTGCGCGCTATGAGTTCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGA	3844
Qy	4712	AAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTCTTCCCATCCCTGC	4771
Db	3845	 AAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCATCCCTGC	3904
Qy	4772	GTGAAGCAGCTTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCA	4831
Db	3905	 GTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTG	3964
Qy	4832	GTGGGAGGG----GGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTT	4887
Db	3965	 TGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCTT	4022
Qy	4888	GCCTCGTGTGACATGAGGCCCATTCTTCACTC----TGAAGAGAGCGGTCACTGTTCTCA	4943
Db	4023	 GCCTCGTGTAAACATGAGGCCCATTCTTCACTCTGTTTGAAGAAAATAGTCAGTGTTCTTA	4082
Qy	4944	GTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATT	5003
Db	4083	 GTAGTGGGTTTCTATTGTTGGATGACTTGGAGATTTATCTCTGTTTCTTTTACAATT	4142
Qy	5004	GTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTTTATGAATG	5063
Db	4143	 GTTGAAATG-TTCCTTTTAATGGATGGTTGAATTAAC TTCAGCATCCAAGTTTATGAATC	4201
Qy	5064	ACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTGTGTTTTATTTCAG	5123
Db	4202	 GTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTAAGAGTCTGTGTTTTATTTCAG	4261
Qy	5124	ATTGGGAAATCCATTCTATTTTGTGAATTGGG---ATAATAACAGCAGTGGAATAAGTAC	5180
Db	4262	 ATTGGGAAATCCGTTCTATTTTGTGAATTGGGACATAATAACAGCAGTGAGTAAGTAT	4321
Qy	5181	TTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAATTAAGAG	5240
Db	4322	 TTAGAAGTGTG---AATTCACCGTGAAATAGGTGAGAT-----AAATTAAGAG	4366
Qy	5241	ATAGTCAATTC TTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATATGCAT	5300
Db	4367	 ATACTTAATTC CGCCTTATGCCTCAGTCTATTCTGTAAAATTTAAAAATATATATGCAT	4426
Qy	5301	ACCTGGATTTCTTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAGAAATTC	5360

```

Db      4427 ACCTGGATTTCTTGGCTTC---GTGAATGTAAGAGAAATTAAATCTGAATAAATAATTC 4483
Qy      5361 TTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAAGGCCCT 5420
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4484 TTTCTGTTAACTGGCTCATTCTTCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCA 4543
Qy      5421 GGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAG 5480
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4544 GGATTAGTAGTGGAGATACTAGGGTAAGCCAGACACACCTACCGATAGGGTATTAAGA 4603
Qy      5481 TCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAA 5540
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4604 GTCTAGGAGCGCGGTCATATAATTAAGGTGACAAGATGTCTCTAAGATGTAGGGAAAA 4663
Qy      5541 GTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGA 5600
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4664 GT----AACGAGTGTGGGTATGGGGCTCCAGGTGAGAGTGGTTCGGGTGTAAATTCCTGT 4719
Qy      5601 GCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGA 5660
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4720 G-TGGGGCCTTTTGGGCTTTGGGAAACTCCATTTTCTTCTGAGGGATCTGATTCTAATGA 4778
Qy      5661 TCTTGGGTGGATCC 5674
      | ||||| |||
Db      4779 AGCTTGGTGGGTCC 4792

```

RESULT 8

ADW41953

ID ADW41953 standard; cDNA; 4895 BP.

XX

AC ADW41953;

XX

DT 24-MAR-2005 (first entry)

XX

DE cDNA elevated in kidney tumor cells SEQ ID NO 1696.

XX

KW gene therapy; diagnosis; pharmaceutical; cancer; cytostatic;

KW genitourinary disease; neoplasm; renal tumor; gene; ss..

XX

OS Unidentified.

XX

PN WO200274237-A2.

XX

PD 26-SEP-2002.

XX

PF 19-MAR-2002; 2002WO-US010055.

XX

PR 19-MAR-2001; 2001US-0277245P.

PR 21-DEC-2001; 2001US-0343340P.

XX

PA (CORI-) CORIXA CORP.

XX

PI Algate PA, Mannion J, Gaiger A, Gordon B, Harlocker SL;

XX

DR WPI; 2002-759855/82.

XX

PT New isolated polynucleotides and polypeptides, useful for detecting the

PT presence of, and treating cancer, particularly kidney cancer by

PT stimulating T-cells specific for a tumor protein, and stimulating immune

PT response in a patient.

XX
PS Claim 13; SEQ ID NO 1696; 252pp; English.

The invention describes a new isolated polynucleotide (I) comprising: any one of the 1855 sequences identified in the specification; complements or degenerate variants of (a); sequences consisting of at least 20 contiguous residues of (a); sequences that hybridize to (a) under highly stringent conditions; or sequences having at least 75 or 90% sequence identity to (a). Also described are: detecting (M1) or determining the presence of cancer in a patient; stimulating (M2) an immune response in a patient; treating (M3) kidney cancer in a patient; an isolated polypeptide (II) encoded by (I) and comprising, or having at least 70 or 90% sequence identity to, any one of the 8 sequences identified in the specification; an expression vector (III) comprising (I) operably linked to an expression control sequence; a host cell (IV) transformed or transfected with (III); an isolated antibody (V) or its antigen-binding fragment that specifically binds to (II); a fusion protein (VI) comprising at least one (II); an oligonucleotide (VII) that hybridizes to the nucleotide sequences cited above under highly stringent conditions; stimulating (M4) and/or expanding T-cells specific for a tumor protein; an isolated T-cell population (VIII) comprising the T-cells in (M4); a composition (IX) comprising a first component such as a carrier or immunostimulant and a second component comprising (I), the polypeptide encoded by (I), an antibody or its antigen-binding fragment that specifically binds to (II), (VI), or an antigen-presenting cell that expresses the polynucleotide; and a diagnostic kit (X) comprising at least one of the oligonucleotide, or at least one antibody and a detection reagent comprising a reporter group. The polynucleotides, polypeptides, antibodies and antigen-presenting cells are useful for detecting the presence of, and treating cancer, particularly kidney cancer by stimulating and/or expanding T-cells specific for a tumor protein, and stimulating immune response in a patient. This sequence represents a kidney tumour cDNA, expression of which is increased in kidney tumors.

SQ Sequence 4895 BP; 1134 A; 1235 C; 1433 G; 1093 T; 0 U; 0 Other;

Query Match 44.3%; Score 2513.6; DB 7; Length 4895;
Best Local Similarity 79.9%; Pred. No. 0;
Matches 3415; Conservative 0; Mismatches 694; Indels 165; Gaps 32;

Qy	1478	ATGGTTC TGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAG	1537
		.	
Db	607	ATAGTCC TGAGGGGCCAGTTGAGATCGGCTGAGGGGAGCGGGCCAAGCTCTGTGGCGAG	666
Qy	1538	GCAAGGTGAGATGCTGAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAA	1597
Db	667	GCAAGGTGAGACTCTGAGGAAGGACTGAGGAGGCCCCACCCAAGATAGA-GGAACCCAA	725
Qy	1598	ATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCGGCCAGGACAGATGTCTCAG	1657
Db	726	ATAATCCAGCCACGTCCTGCTGCCAGTCTCGGACCACCGG---GGGAAGACTTCTCA-	781
Qy	1658	CTGGACCACCCCCGTCCTGCTGCCACTTAACCCACAGGGCAATCTGTAGTCATA	1717
Db	782	---GGCTAGGCCATCCCAGCTCCCCTGCCACTAAAGCTACAGGGGACTCTAGAGTCA--	836
Qy	1718	GCTTATGTGACCGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGC	1777
Db	837	-----AGAGCTTGGTGTGCCCAAGGCAGGGCCAGG	866

Qy	1778	ATCCGCCCGGCATTAGGGTCAGGACCCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCT	1837
Db	867	CTCTGCCTGGCATCGGGGTCAAGACCTTGAGAGGGAACCTGAGGGCGCTACACCCCCACCC	926
Qy	1838	GTCCTCTCATCTCCACCGCCACCCCACTCACAATTCCTACCCCTACCCCCAACC	1897
Db	927	CATCCGCATTC-----CAACATGCCAGCCCCATCCCCAACTCCGTTTTGCAGAA	976
Qy	1898	TCATCTTGTGAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCAC	1957
Db	977	TCCATTTTTT----TCCCCTGCAGTCAACCCCGGGAAGACCTGGGAATGGT---CAGGCAC	1029
Qy	1958	TCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAACAG	2010
Db	1030	TCGGATCTTGACATCCACATCGAGGGCTGAAGGAGGGAGAGAGTTTGGTATCATGAGCAG	1089
Qy	2011	GGCCTCAGGGGAGCAGAGGGAG-----GGCCCTACTGCGAGATGAGGGAGGCCTCAGAG	2064
Db	1090	AGCCTCAGGGTAGCAGAGGGAGGACCCTGGCCCTCTGGGAGATGAGGAAGGCCTCAGGA	1149
Qy	2065	GACCCAGCACCC-----TAGGACACCGCACCCCTGTCTGAGACTGAG--GCTGCCA	2113
Db	1150	GACCCAGCACCCCAAGGCAGGGAGCCACCCACCCCTGTCTGAGAATGAGGTGCCTCCT	1209
Qy	2114	CTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGA--CCCAG	2171
Db	1210	CCTTTAGCCTCAGGAATCCAAGGGATGGCAACTCAGGTCAGCAGAGGGGTGGGTTCACAG	1269
Qy	2172	GCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGAATCCAGAT	2231
Db	1270	CCCTTCCAGGATCAAGGAAAGGAAGACGAGGGAGGATTTCAGGGGGCCTTGCATTCCAGAT	1329
Qy	2232	CAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTTC	2291
Db	1330	CAGTGGAGACCTGGGCCCTGGGAGGTCTGGGCAAGGTAGCCACCTGTAGCTCATACTTC	1389
Qy	2292	CTGCATCTTTGAGGT----GACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTC	2347
Db	1390	CTGCATCTTCGAGGTCACAGAGAGGAGAGGGCTATGGTCTGAGGGGTGGTACTTCAGGTC	1449
Qy	2348	AACAGAGGGAGGAGTTCCAGGATCCATATGGCCCCAAGATGTGCC--CCCTTCATGAGGACT	2406
Db	1450	CGCAGAGGGAGGAGTCCAGGATCTACAGGACCCAAGGTGTGCCACACTTCACGAGGAAT	1509
Qy	2407	GGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTTTTAGTA	2466
Db	1510	GGGGATACCTGTGGCTCAGAAAGACGGGACCCACAGAGTCTGGCTGTCCCTGTCTCTTA	1569
Qy	2467	GCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCA	2526
Db	1570	GCTCAGGGGGGACCAGAGGAGGGATGGCCCTATGTGCCAATTTCATTGTTCCACAGGCA	1629
Qy	2527	GGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCAT	2586
Db	1630	GGAAGTTGGGGAACCTTCAGGGAGATGAGGTTTTGGAGTAAAGGGGCAATGTTTGCTCAT	1689
Qy	2587	GTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACA	2646
Db	1690	CTCAGGGGGTTGGGGGTTGAGGAAGGACAGGCCCTGTCAGGAGCAACATGAGT-ACCCA	1748
Qy	2647	GACAAGGCTATTGGAATCCACACCCAGAACCAAGGGGTGAGCCCTGGACACCTCACCC	2706

Db	1749	CAGGAGGCCATCAGAACCCCTCACCCCAGAACCAAAGGGGTCAGCCCTGGGCACCCCACAC	1808
Qy	2707	AG-----GATGTGGCTTCTTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGAC	2758
Db	1809	AGGGGTGACAGGATGTGGCTCCTTCTCATTTCTGATTCCAGATCTCAGTGAGGTGAGGAC	1868
Qy	2759	CTCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAG	2818
Db	1869	CTTGTTCTCAGAGGGTGACTCAGGTCAACACAGGGACCCCCATCTGGTCTACAGACACAG	1928
Qy	2819	CGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCC	2878
Db	1929	TGGTCCCAGGATCTGCCAAGAGTCCTGGTGAGGAATGTGAGGGAGGATTGAGGGTACCAC	1988
Qy	2879	AGGACCAGAACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCCAG	2938
Db	1989	AGGGCCAGAACGCAGATGATGACCCACAGAAATCAGCCCTGCTCCTGTTGTCACCCCAG	2048
Qy	2939	AGAGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAG	2998
Db	2049	AGAGCATGGGCTTGGCTTTCTGCTGAGGTCCCTCTCTTATCCTGGGATCACTGGTGTCAC	2108
Qy	2999	GGACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGG	3058
Db	2109	GGAGGGGGAGGCCCTTGGTCTGAGGGGGCTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGG	2168
Qy	3059	CCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCA	3118
Db	2169	CTCTGCCAGGAGTTGAGGTGAGGACCAAGCAGGCTCCGCATCCAGGACACATGGGTTCCA	2228
Qy	3119	ATGAATTTTGATATCTCTTGCTGCCCTTC-CCCAAGGACCTAGGCACGTGTGGCCAGATG	3177
Db	2229	ATGAATTTTGACATCTTTTGCTGTCGTTCTTCGGAAGACCTAGGCACAGGTGGCCAGATG	2288
Qy	3178	TTTGTCCCTCCTGTCTTCCATTCTTATCATGGATGTGAACCTTGATTGGATTCT	3237
Db	2289	TGGGGTTTCTTAGGTCCT---GTTCCCTCTCAGGCATGTGAGCTCTTGATCTGAGTTTCT	2345
Qy	3238	CAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGA	3297
Db	2346	CAGGCCAGCAAAAGAGTGGGATCCAGGCCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGA	2405
Qy	3298	GAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTC	3357
Db	2406	ACACAGTGGGGATCATCCACTCCATGAGAGTGGGGACCTCACAGAGTCCAGCCTACCTC	2465
Qy	3358	CTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGATT	3417
Db	2466	TTGATGGCACTGAGGGACCGGGCTGTGCTTACAGTCTGCACCTAAGGGCCCATGGATT	2525
Qy	3418	CCTCTTCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAG	3477
Db	2526	CCTCTCTAGGAGCTCCAGGAACAAGGCAGTGAGGCCTTGGTCTGAGACAGTGTCTCAG	2585
Qy	3478	GTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACAC	3537
Db	2586	GTTACAGAGCAGAGGATGCACAGGCTGTGCCAGCAGTGAATGTTGCCCTGAATGCACAC	2645
Qy	3538	CAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTA	3597

Db 2646 CAAGGGCCCCACCTGCCACAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCTCCCTA 2705

Qy 3598 CTGTCAGTCCTGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACT 3656
| ||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 2706 CCATCAATCCTGCAGAATCGACCTCTGCTGGCCGGCTATACCCTGAGGTGCTCTCTCACT 2765

Qy 3657 TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC 3716
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 2766 TCCTCCTTCAGGTTCTGAGCAGACAGGCCAA-CCGGAGGACAGGATTCCCTGGAGGCCAC 2824

Qy 3717 AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT 3776
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 2825 AGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCTAAGATTGGT 2884

Qy 3777 TCTCAGCTGAGGCCCTCTCACACACTCCCTCTCTCCCCAGGCCGTGGGTCTTCATTGCC 3836
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 2885 TCTCAGCTGAGGTCTCTCACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCC 2944

Qy 3837 AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA 3896
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 2945 AGCTTTTGCCCTGCACCTCTTGCCCTGCTGCCCTGAGCAGAGTCATCATGTCTCTTGAGCAGA 3004

Qy 3897 GGAGTCTGCAC TGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG 3956
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 3005 AGAGTCAGCACTGCAAGCCTGAGGAAGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGG 3064

Qy 3957 TGTGTGTGCAGGCTGCCAC-----CTCCTCCTCCTCTCCTC 3992
| | ||| |||| | || | |||| | |||| | |||| | |||| | |||| | |||| |

Db 3065 TGGGTGCGCAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTC 3124

Qy 3993 TGGTCCTGGGCACCC TGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTC 4052
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 3125 TGGTCCCTGGCACCCTGGAGGAAGTGCTGCTGCTGAGTCAGCAGGTCTCCCCAGAGTC 3184

Qy 4053 CTCAGGGAGCCTCCGCCCTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTG 4112
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 3185 CTCAGGGAGCCTCTGCCCTTACCACTACCATCAGCTTCACTTGCTGGAGGCAACCCAATG 3244

Qy 4113 AGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGT 4172
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 3245 AGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAGTCCTTGT 3304

Qy 4173 TCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATC 4232
| |||| | ||| || | ||| || | |||| | ||| || | |||| | ||| || | |||| |

Db 3305 TCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTATC 3364

Qy 4233 GAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGC 4292
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 3365 GAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAGC 3424

Qy 4293 ACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTG 4352
| || | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 3425 GCTGCTTTCTTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTG 3484

Qy 4353 ACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCT 4412
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 3485 ACGTGAAGGAAGTGACCCACAGCAACACCTACACCTTGTACCTGCCTGGGCCTTT 3544

Qy 4413 CCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCTGATAATTG 4472
| |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |

Db 3545 CCTATGATGGCCTGCTGGGTGATAATCAGATCTTTCCCAAGACAGGCTTCTGATAATCG 3604

Qy	4473	TCCTGGTTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGC	4532
Db	3605	TCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGC	3664
Qy	4533	TGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGC	4592
Db	3665	TGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAAAC	3724
Qy	4593	TGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTG	4651
Db	3725	TGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTACCCGGCAGTA	3784
Qy	4652	ATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGA	4711
Db	3785	ATCCTGCGCGCTATGAGTTCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGA	3844
Qy	4712	AAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGC	4771
Db	3845	AAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATTGCCTACCCATCCCTGC	3904
Qy	4772	GTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCA	4831
Db	3905	GTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTG	3964
Qy	4832	GTGGGAGGG----GGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTT	4887
Db	3965	TGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCTT	4022
Qy	4888	GCCTCGTGTGACATGAGGCCCATTTCTTCACTC----TGAAGAGAGCGGTCAGTGTTCTCA	4943
Db	4023	GCCTCGTGTAAACATGAGGCCCATTTCTTCACTCTGTTTGAAGAAAATAGTCAGTGTTCTTA	4082
Qy	4944	GTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATT	5003
Db	4083	GTAGTGGGTTTCTATTTTGTGATGACTTGGAGATTTATCTCTGTTTTCCTTTTACAATT	4142
Qy	5004	GTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTTTATGAATG	5063
Db	4143	GTTGAAATG-TTCCTTTTAATGGATGGTTGAATTAACCTTCAGCATCCAAGTTTATGAATC	4201
Qy	5064	ACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTGTGTTTTATTTCAG	5123
Db	4202	GTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTAAGAGTCTGTGTTTTATTTCAG	4261
Qy	5124	ATTGGGAAATCCATTCTATTTTGTGAATTGGG---ATAATAACAGCAGTGGAATAAGTAC	5180
Db	4262	ATTGGGAAATCCGTTCTATTTTGTGAATTTGGGACATAATAACAGCAGTGAGTAAGTAT	4321
Qy	5181	TTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAG	5240
Db	4322	TTAGAAGTGTG---AATTACCGTGAAATAGGTGAGAT-----AAATTAAG	4366
Qy	5241	ATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGCAT	5300
Db	4367	ATACTTAATTCCTGCTTATGCCTCAGTCTATTCTGTAAAATTTAAAAATATATATGCAT	4426
Qy	5301	ACCTGGATTTCCTTGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAGAATTC	5360
Db	4427	ACCTGGATTTCCTTGCTTCT---GTGAATGTAAGAGAAATTAATCTGAATAAATAATTC	4483

```

Qy      5361 TTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGGAAGGCCCT 5420
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4484 TTTCTGTTAACTGGCTCATTCTTCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCA 4543

Qy      5421 GGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAG 5480
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4544 GGATTAGTAGTGGAGATACTAGGGTAAGCCAGACACACCTACCGATAGGGTATTAAGA 4603

Qy      5481 TCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAA 5540
        |  |  |||  |||  ||||| ||||| ||||| ||||| ||||| |||||
Db      4604 GTCTAGGAGCGCGGTCATATAATTAAGGTGACAAGATGTCCTCTAAGATGTAGGGAAAA 4663

Qy      5541 GTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGA 5600
        ||  |  |  |||  ||||| ||||| ||||| ||||| ||||| |||||
Db      4664 GT----AACGAGTGTGGGTATGGGGCTCCAGGTGAGAGTGGTCGGGTGTAAATTCCTGT 4719

Qy      5601 GCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGA 5660
        |  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4720 G-TGGGGCCTTTTGGGCTTTGGGAAACTCCATTTTCTTCTGAGGGATCTGATTCTAATGA 4778

Qy      5661 TCTTGGGTGGATCC 5674
        |  ||||| |||
Db      4779 AGCTTGGTGGGTCC 4792

```

RESULT 9

ABQ76206

ID ABQ76206 standard; DNA; 4736 BP.

XX

AC ABQ76206;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human tumour antigen MAGE-5b DNA.

XX

KW Tumour antigen; human; vaccine; cellular immune response; immunogen;

KW cancer; tumour; MAGE-5b; ds.

XX

OS Homo sapiens.

XX

PN US6287569-B1.

XX

PD 11-SEP-2001.

XX

PF 06-APR-1998; 98US-00056105.

XX

PR 10-APR-1997; 97US-0043467P.

XX

PA (REGC) UNIV CALIFORNIA.

XX

PI Kipps TJ, Wu Y;

XX

DR WPI; 1998-583198/49.

XX

PT Generating cellular immune response in patient to target protein -

PT comprises introducing vector with nucleotide sequence encoding immunogen

PT comprising protein processing signal into cell of patient.

XX

PS Disclosure; Col 54-58; 6lpp; English.

XX

CC This invention describes a novel method for generating a cellular immune

CC response in a patient to a target protein or its fragment. The method
 CC involves introducing a vector containing a nucleotide sequence encoding a
 CC chimeric immunogen comprising a protein processing signal and the target
 CC protein or its fragment. The immunogen is produced by the cells and
 CC processed so that the target protein or its fragment is presented to the
 CC patients immune system and a cellular immune response is initiated. The
 CC method and vectors can be used as a form of vaccination and could be used
 CC to generate a cellular immune response in patients to, e.g. cancerous
 CC tumours. The cellular immune response is the predominant immune response
 CC in the patient. This sequence represents a DNA fragment which encodes the
 CC human tumour antigen MAGE-5b described in the method of the invention.
 CC Note: The information in this spec has been previously disclosed in
 CC WO199845444 however this spec contained no sequence information

XX

SQ Sequence 4736 BP; 1114 A; 1278 C; 1304 G; 1040 T; 0 U; 0 Other;

Query Match 42.8%; Score 2429.6; DB 2; Length 4736;
 Best Local Similarity 75.9%; Pred. No. 0;
 Matches 3736; Conservative 0; Mismatches 869; Indels 315; Gaps 47;

```

Qy      715 TTCCCGCCAGGAACATCCGGGTGCCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGG 774
          ||| |||| || | |||| || |||| |||| |||| |||| |||
Db      15 TTCAACCCAGGGAATCCCTGGGTGACCAGATGTGGTGCCACTGTCTTGACATTGAGGT 74

Qy      775 CAGAGAGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGA 834
          | |||| |||| || | ||| |||| | || | ||| || | |||
Db      75 CGGAGAGAAGCAAGGGCCTCGCTCTCAGGGGCAGC-TGGAGATCAGCTGAGGGCAGCTGG 133

Qy      835 CCCAGGCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTC 894
          ||| |||| |||| || |||| |||| |||| |||| |||| |||
Db      134 CCCTGGCTCTGTGAGGATGCAAGGTGAGATGCTGAGGGAGGACTAAGGAGTATCCACCC 193

Qy      895 CAAATAGAGAGCCCCAAATATTCCAG---CCCCGCCCTTGCTGCCAGCCCTGGCCACCC 951
          | ||| | |||| |||| || | || | |||| || |||| |||
Db      194 CTGGTAGTGACCCCAAATAATCCAGTGCCACCTCTCCTGCTGCTAGCTCTGGACCATCC 253

Qy      952 GCGGGAAGACGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGAC 1011
          || | ||| || | |||| |||| |||| ||| | | |||| | ||
Db      254 AGGGCAGGACTTCTTAGGCTGGGCCACCCCCAGTCCCCCACCCTTAAGCCGCAGGGGA- 312

Qy      1012 ACCAGGTTCTTCTCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGT 1071
          ||| ||| |||| ||| | |||| |||| |||| ||||
Db      313 -----CTCAGGAGACAGAGCTTGGTATGACCAGGGCAGGACTGGT 352

Qy      1072 TAGGAGAGGGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGC 1131
          |||| |||| || | || |||| |||| || ||| ||| ||| |||
Db      353 TAGGAGAGGACAGCTCCA-GCTCTGCCAGGAAACAACGTCAGGAACCTAAGGGAAAGCT 411

Qy      1132 TGTGGGCCCCCAAGACTGCACTCCAATCCCCACTCCACCCCATTCGCATTCCCATTTCCC 1191
          | ||||
Db      412 GAGGCTACCCC----- 422

Qy      1192 CACCCAACCCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCAC 1251
          |||| | | | | || ||| |||| | |
Db      423 -----CACCCAAACTCTATTCTGTCCCTACCTCCGTCC 457

Qy      1252 CTGACCACCACCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCCTCACT 1311
          | ||| |||| || || || |||| |||| | | |||| | |||
Db      458 CCCACCTACACCCCATTC-----CCACCCCTTCCCTACCGGCACCTCTATCCACACA 512

Qy      1312 GCCCCCAACCCACCCCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTTCTG 1371

```

```

      |||||
Db      513 TCCCCCA-----CCCCTATCCTG 530
Qy      1372 GCAGAAATCCGGTT-TGCCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAA 1430
      ||||| || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      531 GCAGAAATCCGATTCTGCCCCGTGATTTCAACCCAGGGAAGCCCTAGGGGGCCGGATGTGAT 590
Qy      1431 ACCACTGACTTGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTTAATGGTTCTGAGGG 1490
      | ||||| || || ||||| || || ||||| |||||
Db      591 GCTGCTGACTTGTGCATTGGGGGTCAGAGAGAATCAAGG-----GCATGGTTCTGAGAA 644
Qy      1491 GCGGCTTGAGATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATG 1550
      || | ||||| || ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Db      645 GCCGACTGAGATCAGCAGAGGGGAATGGGCCCGGGCTCTGTGAGGAGGCAAGGTGAGACC 704
Qy      1551 CT-GAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTAC 1609
      | |||| |||| ||||| || ||||| || || ||||| ||||| ||||| |||||
Db      705 CCCGAGGAAGGAATGAGGAAGCCCTCACCC--AGATAGAGAACCCCAAATAATCCAGTAC 762
Qy      1610 CACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCC 1669
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      763 TACCTCTGCTGCCAGCCCTGGACCAC----CCAGGCAGACTTCTCAGGCTGAACCTTCC 818
Qy      1670 CCGTCCCCTGCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTT-ATGTGAC 1728
      | |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      819 C---CCCTCCCCACTGCCACTTAAGCCACAAGGGACTCTGGAGTCAGACCTTGGTGTGAC 875
Qy      1729 CGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGC 1788
      | |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      876 CAGGGAAGGGCCGGTCAGGAGAGG-----GCAGGGGCCAGGCTCTGTCTAGGC 922
Qy      1789 ATTAGGGTCAGGACCTGGGAGGGAACCTGAGGGTTCCCCACCCACACCTGTCTCCTCATC 1848
      || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      923 ATCAAAATCAGGACCTGAGAGAGAATTGAGGGCCCCACCCCAACCCCTATACCCATCC 982
Qy      1849 TCCACCGCCACCCCACTCACATTCCCATACCTACC----CCCTACCCCCAACCTCATCTT 1904
      ||| | ||||| || || ||||| || || ||||| ||||| ||||| ||||| |||||
Db      983 CTAACCCCATACCCACTCTACTTGCATTCCAGCCCCATCCCCACACCCCTACCCCATCTT 1042
Qy      1905 GTCAGAA-----TCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGG 1954
      | |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1043 GGCAGAATCTGTTCTTTCCCTGCAGTCAACCCACAGAAGCCCCAGGAATGACAGACAGG 1102
Qy      1955 CACTCGGATCTTGACGTCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAA 2007
      ||| | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1103 CACACCATCTTGACGTCCACATCCAGGGCTGAAGGAGGGAAGGGCTTAGTATCATGAG 1162
Qy      2008 CAGGGCCTCAGGGGAGCAGAGG----GAGGGCCCTACTGCGAGATGAGGGAGGCCCTCAGA 2063
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1163 CAGGGCCTCAGGGGAGTCTCTGCTCCTCAAGCCCTGCTGGGAGTAAAGGGAGGCCCTCAGG 1222
Qy      2064 GGACCCAGCACCCCTAGGA-----CACCGCACCCCTGTCTGAGACTGAGGC--TGCC 2112
      | ||||| || ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
Db      1223 GAACCCAGGTCCTCAGGATAGGGGGTCCACTCCAACCCTGTCTGAGACTGAGGCGCCTCC 1282
Qy      2113 ACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGACCCAGG 2172
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1283 TCTTTCATCCTCGGGAATCACAGGGATGGAGACTCACGTCAGCAGAGGGTGGGGCCCAAC 1342
Qy      2173 CCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGAATCCAGATC 2232
      ||||| ||| | | ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Db 1343 CCTGCCAGGATCAAGGAGAGGAAGAAGAGGGAGGACTCAGGGTACCTTTGAGTCCAGAAC 1402

Qy 2233 AGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTCC 2292
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1403 AATGGGGACCTTTGCCCTGGGAGGTCCAGTGCACAGTGGCCACCTGTAGCCCATGCTTGC 1462

Qy 2293 TGCATCTTTGAGGTGAC----AGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCA 2348
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1463 TGCACCTTCTGGGTGACAAAGAGGAGAGGGCTGTGGTCAGAGCAGTGGTGACTCAGGTCA 1522

Qy 2349 ACAGAGGGAGGAGTTCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATGAGGACTGG 2408
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1523 GCAGAGGGAGGAGTCCCAGCATCTGCAGGCCCAATGTGTGCCCCATTCATGAAGATTGG 1582

Qy 2409 GGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTTTTAGTAGC 2468
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1583 GGACA-CCTTGGCTCAGAAAGAAGGGACCCACAGAGTCTGGCTGTCCCCTGATTTTTGC 1641

Qy 2469 TCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCAGG 2528
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1642 TCAGAGGGGACCAAATCAAGGATAGCCCTATGTGCCAACCTCATTTGTGCCACAGGAAAG 1701

Qy 2529 AAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGT 2588
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1702 AAGTTGAAGAGCCCTCAGGGTGATGGGGTCTTGACAGTAAAGGGGAGCTATCTGCTCATCT 1761

Qy 2589 CAGGGAATTGGGGGTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGA 2648
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1762 CAGGGGGTTTCAGGTTGAGGAATGGCAGGCCCATCACGATGAAGAGTAACCCACAGG-- 1819

Qy 2649 CAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGACACCTCA----- 2703
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1820 ---AGCCATAGAAACACTCACCCCAGAACCAAAGGGGTCATACCTGGACACCCCATGTGG 1876

Qy 2704 ----CCCAGGATGTGGCTTCTTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACC 2759
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1877 GGGTGACAGGATGTAGCT-CCATCTCATTCCTGTTTTCAGATCTCGGGGAGGTGAGGAAC 1935

Qy 2760 TCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGC 2819
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1936 TTGTTCTCCGAGGATGACTCAGGTCAACACAGGGGCCCCCATCTGGTGGATAGACAGAGT 1995

Qy 2820 GGTCCCAGGATCTGCCATGCGTTCCGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCA 2879
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1996 GGTCCCAGGATCTGTCAGTAGTTCCGGTGAGGAACATGAGGGACGATTGAGGGCACCTT 2055

Qy 2880 GGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCCCAGA 2939
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 2056 GGGCCAGAACACAGATGAGGACCTCACGGAATCTGCCCTGCCCTGCTGTCACTCCAGA 2115

Qy 2940 GAGCATGGGCTGGGCCGTCTGCCGAGGTCTTCC--GTTATCCTGGGATCATTGATGTCA 2997
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 2116 GAGCATGGGCAGGGCTGTCTGCTGCAGTCCCCCCCATTACCCTGGGATCATTGGTGTCA 2175

Qy 2998 GGGACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAG 3057
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 2176 GTGATGGGGAGGTCTTTGTC-GAGGGGTCTGCACTCAGGTCAGTAGAGGGAGCGTCTTAG 2234

Qy 3058 GCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTACCCAGGACACATTAATTCC 3117
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 2235 GCCCTGCCAGGAGACAAGGTAAGAACGAAGCAGGTTCTCACCAGGACACATGAATTCC 2294

Qy	3118	AATGAATTTTGATATCTCTTGCTGCCCTTCCCCA-AGGACCTAGGCACGTGTGGCCAGAT	3176
Db	2295	AATGCATTTTCAGCATCTCTTCTGTCCTTCCCAAGAGGACCTGGGCACGTGTGGCCAGAT	2354
Qy	3177	GTTTGTCCCCTCCTGTCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTGATTTC	3236
Db	2355	GTGAGTCTCCTCATGTCTCT---GTTCCCTATCAGGGATGTGAGCTCTTAATCTGAGTTTC	2411
Qy	3237	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	3296
Db	2412	TCAGGCCAGCAAAAGGGTGGGATCCAGGCCCTGCCAGGAGAAAGGTGAGGGCCCTGTGTG	2471
Qy	3297	AGAACAGAGGGGGTTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCT	3356
Db	2472	AGCACAGAGGGGACCATTCACCCCAAGAGGGTGGAGACCTCACAGATTCCAGCCTACCT	2531
Qy	3357	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT	3416
Db	2532	CCTGTTAGCACTGGGGGCTGAGGCTGTGCTTGCACTCTGCACCCTGAGGGCCCATGCAT	2591
Qy	3417	TCCTCTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCA	3476
Db	2592	TCCTCTTCCAGGAGCTCCAGGAAACAGACACTGAGGCCCTGGTCTGAGGCCGTGCCCTCA	2651
Qy	3477	GGTCACAGAGCAGAGGATGCACAGGGT---GTGCCAGCAGTGAATGTTGCCCTGAATG	3532
Db	2652	GGTCACAGAGCAGAGGAGATGCAGACGTCTAGTGCCAGCAGTGAACGTTGCCCTGAATG	2711
Qy	3533	CACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCA-CC	3591
Db	2712	CACACTAATGGCCCCCATCGCCCCAGAACATATGGGACTCCAGAGCACCTGGCCTCACCC	2771
Qy	3592	TCCCTACTGTGAGTCTGTAGAACGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTC	3651
Db	2772	TCTCTACTGTGAGTCTGTGAGAATCAGCCTCTGCTTGCTTGCTGTACCCTGAGGTGCCCTC	2831
Qy	3652	TCACTTCCTCCTTCAGGTTTTCAGGGGACAGGCCAACCCAGAGGAC-----A	3698
Db	2832	TCACTTTTTCCTTCAGGTTCTCAGGGGACAGGCTGACCAGGATCACCAGGAAGCTCCAGA	2891
Qy	3699	GGATTCCCTGGAGGCCACAGAGGAGCACC-AAGGAGAAGATCTGTAAGTAGGCCTTTGTT	3757
Db	2892	GGATCCCCAGGAGGCCCTAGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTT	2951
Qy	3758	AGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGC	3817
Db	2952	AGAGCCTCCAAGGTTTCAGTTTTCAGCTGAGGCTTCTCACATGCTCCCTCTCTCTCCAGGC	3011
Qy	3818	CTGTGGGTCTTCATTGCCAGCTCCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTC	3877
Db	3012	CAGTGGGTCTTCATTGCCAGCTCCTGCCACACTCCTGCCTGTTGCGGTGACCAGAGTC	3071
Qy	3878	ATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCCAA	3937
Db	3072	GTCATGTCTCTTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGCCCTTGACACCAA	3131
Qy	3938	CAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC-----C	3976
Db	3132	GAAGAGGCCCTGGGCCTGGTGGGTGTGCAGGCTGCCACTACTGAGGAGCAGGAGGCTGTG	3191

Qy	3977	TCCTCCTCCTCTCCTCTGGTCTCGGGCACCCCTGGAGGAGGTGCCCACTGCTGGGTCAACA	4036
Db	3192	TCCTCCTCCTCTCCTCTGGTCCCAGGCACCCTGGGGGAGGTGCCTGCTGCTGGGTACCA	3251
Qy	4037	GATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACCTCGA	4096
Db	3252	GGTCCCTCTCAAGAGTCCTCAGGGAGCCTCCGCCATCCCCACTGCCATCGATTTCACCTCTA	3311
Qy	4097	CAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGT	4156
Db	3312	TGGAGGCAATCCATTAAGGGCTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTCCCT	3371
Qy	4157	ATCCTGGAGTCCTTGTTCAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTT	4216
Db	3372	GACCCAGAGTCTGTGTTCCAGCAGCACTCAGTAAGAAGGTGGCTGACTTGATTCATTTT	3431
Qy	4217	CTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTC	4276
Db	3432	CTGCTCCTCAAGTATTAAGTCAAGGAGCCGGTCACAAAGGCAGAAATGCTGGAGAGCGTC	3491
Qy	4277	ATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAG	4336
Db	3492	ATCAAAAATTACAAGCGCTGCTTTCTGAGATCTTCGGCAAAGCCTCCGAGTCCTTGCAG	3551
Qy	4337	CTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCAGCCACTCCTATGTCCTTGTC	4396
Db	3552	CTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCAGCAACACCTACACCCTTGTC	3611
Qy	4397	ACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACA	4456
Db	3612	ACCTGCCTGGG--ACTCCTATGATGGCCTGGTGGTT--TAATCAGATCATGCCCAAGACG	3667
Qy	4457	GGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAG	4516
Db	3668	GGCCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAAATGCGTCCCTGAGGAG	3727
Qy	4517	GAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTAT	4576
Db	3728	AAAATCTGGGAGGAGCTGGGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGT	3787
Qy	4577	GGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGC	4636
Db	3788	GGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGC	3847
Qy	4637	AGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCTG	4696
Db	3848	AGGTGCCCAGCAGTGATCCCATATGCTATGAGTTACTGTGGGGTCCAAGGGCACTCGCTG	3907
Qy	4697	AAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTT	4756
Db	3908	CT-----TGAAAGTACTGGAGCACGTGGTCAGGGTCAATGCAAGAGTTCTCATTT	3957
Qy	4757	TCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAG	4816
Db	3958	CCTACCCATCCCTGCATGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAG	4017
Qy	4817	TTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAG	4876
Db	4018	CTGCAGCCAGGGCCACTGCGAGGGGGGTGGGCCAGTGCACCTTCCAGGGCTCCGTCCAG	4077
Qy	4877	CAGCTTCCCTGCC--TCGTGTGACATGAGGCCCATTCCTTCACTC--TGAAGAGAGCGGTC	4933

```

      || ||||| ||| | ||||| ||||| ||| ||||| |||
Db      4078 TAGTTTCCCTGCCTTAATGTGACATGAGGCCATTCTCTCTCTTTGAAGAGAGCAGTC 4137
Qy      4934 AGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTC 4993
      | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||
Db      4138 AACATTCTTAGTAGTGGGTTTCTGTTCTATTGGATGACTTTGAGATTTGTCTTTGTTTCC 4197
Qy      4994 TTTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAG 5053
      ||||| ||||| ||| ||||| ||| ||||| ||||| ||||| |||
Db      4198 TTTTGGAATTGTTCAAATG-TTCCTTTTAATGGGTGGTTGAATGAACTTCAGCATTCAA 4256
Qy      5054 TTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTG 5111
      ||||| ||||| ||||| ||| ||||| ||||| ||| ||||| |||
Db      4257 TTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCTTG 4316
Qy      5112 TGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAGCAGT 5169
      | ||||| ||||| ||||| ||||| ||||| ||||| ||| | |||||
Db      4317 TTTTTTATTTCAGATTGGGAAATCCATTCCATTTTGTGAATTGGGACATAGTTACAGCAGT 4376
Qy      5170 GGAATAAGTACTTA-GAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAA 5228
      ||||| ||| | | ||||| ||||| ||||| |||
Db      4377 GGAATAAGTATTCATTTAGAAATGTGAATGAGCAGTAAACTGATGAGA-----TAA 4428
Qy      5229 AGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAA--TTTTT 5286
      ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||
Db      4429 AGAAATTAAGAGATATTTAATTCTTGCCTTATA-CTCAGTCTATTCGGTAAATTTTTTT 4487
Qy      5287 AAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATC 5346
      | | || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4488 TTAAAAATGTGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGACAAATTAAATC 4547
Qy      5347 TGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCT 5406
      ||||| ||||| ||||| ||||| ||||| ||| ||||| ||||| |||||
Db      4548 TGAATAAATCATTCTCCCTGTTCACTGGCTCATTTATTCTCTATGCACTGAGCATTTGCT 4607
Qy      5407 TTTTGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCC 5466
      | ||||| ||||| ||||| ||||| ||||| ||||| ||| |||||
Db      4608 CTGTGGAAGGCCCTGGGTTAATAGTGGAGATGCTAAGGTAAGCCAGACTCACCCCTACCC 4667
Qy      5467 ATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAA 5526
      | |||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4668 ACAGGGTAGTAAAGTCTAGGAGCAGCAGTCATATAATTAAGGTGGAGAGATGCCCTCTAA 4727

```

RESULT 10

ABQ76205

ID ABQ76205 standard; DNA; 4741 BP.

XX

AC ABQ76205;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human tumour antigen MAGE-5a DNA.

XX

KW Tumour antigen; human; vaccine; cellular immune response; immunogen;

KW cancer; tumour; MAGE-5a; ds.

XX

OS Homo sapiens.

XX

PN US6287569-B1.

XX


```

Db      313 -----CTCAGGAGACAGAGCTTGGTATGACCAGGGCAGGACTGGT 352
Qy      1072 TAGGAGAGGGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGC 1131
      ||||| ||| | || ||||| ||| | ||| | ||| |
Db      353 TAGGAGAGGACAGCTCCCA-GCTCTGCCAGGAAACAACGTCAGGAACCTAAGGGAAAGCT 411
Qy      1132 TGTGGGCCCCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTTCCATTCCC 1191
      | |||
Db      412 GAGGCTACCCC----- 422
Qy      1192 CACCCAACCCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTCAC 1251
      |||| | | | | ||| ||| |||| | |
Db      423 -----CACCCAAACTCTATTCTGTCCCTACCTCCGTCC 457
Qy      1252 CTGACCACCACCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCTCACT 1311
      | ||| |||| | || | || ||| ||| | |||| | |||
Db      458 CCCACCTACACCCCATTC-----CCACCCCTTCCCTACCGGCACCTCTATCCACA 512
Qy      1312 GCCCCAACCCACCTCATCTCTCTCATGTGCCCACTCCCATCGCCTCCCCATTCTG 1371
      ||||| |||| | |||
Db      513 TCCCCA-----CCCCTATCCTG 530
Qy      1372 GCAGAATCCGGTT-TGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCGATGTGAA 1430
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      531 GCAGAATCCGATTCTGCCCTGATTTCAACCCAGGGAAGCCCTAGGGGGCCGGATGTGAT 590
Qy      1431 ACCACTGACTTGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCTGAGGG 1490
      | ||||| | | || ||||| | || | |||||
Db      591 GCTGCTGACTTGTGCATTGGGGGTCAGAGAGAATCAAGG-----GCATGGTTCTGAGAA 644
Qy      1491 GCGGCTTGAGATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATG 1550
      || | ||||| | ||||| ||| ||||| ||||| ||||| |||||
Db      645 GCCGACTGAGATCAGCAGAGGGGAATGGGCCCGGGCTCTGTGAGGAGGCAAGGTGAGACC 704
Qy      1551 CT-GAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTAC 1609
      | |||| |||| ||||| || | |||| | | || |||| |||||
Db      705 CCCGAGGAAGGAATGAGGAAGCCCTCACCC--AGATAGAGAACCCCAAATAATCCAGTAC 762
Qy      1610 CACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCC 1669
      ||| ||||| ||||| ||||| ||||| ||||| ||| ||
Db      763 TACCTTTGCTGCCAGCCCTGGACCAC----CCAGGGCAGACTTCTCAGGCTGAACCTTCC 818
Qy      1670 CCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTT-ATGTGAC 1728
      | ||| ||||| ||||| ||||| || | ||| |||| | ||| |||||
Db      819 C---CCCTCCCACTGCCACTTAAGCCACAAGGGACTCTGGAGTCAGACCTTGGTGTGAC 875
Qy      1729 CGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCCGC 1788
      | ||| |||| ||||| ||||| || || |||| || | |||
Db      876 CAGGGAAGGGCCGGTCAGGAGAGG-----GCAGGGGCCAGGCTCTGTGAGGC 922
Qy      1789 ATTAGGGTCAGGACCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCATC 1848
      || | ||||| |||| || ||||| || |||| || ||| |
Db      923 ATCAAAATCAGGACCTGAGAGAGAATTGAGGGCCCCACCCCAACCCCTATACCCATCC 982
Qy      1849 TCCACCGCCACCCACTCACATTCCCATACCTACC----CCCTACCCCAACCTCATCTT 1904
      ||| | ||||| || | || || || ||| || ||| |||||
Db      983 CTAACCCATACCACTCTACTTGCATTCCCAGCCCATCCCACACCTACCCATCTT 1042
Qy      1905 GTCAGAA-----TCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGG 1954
      | |||| ||||| ||||| ||||| ||||| | |||| | |||
Db      1043 GGCAGAATCTGTTTCTTTCCCTGCAGTCAACCCACAGAAGCCCCAGGAATGACAGACAGG 1102

```

Qy 1955 CACTCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAA 2007
 ||| | || ||||| ||||| | | ||| | |||
 Db 1103 CACACCTATTCTGACGTCCACATCCAGGGCTGAAGGAGGGAAGGGCTTAGTATCATGAG 1162

Qy 2008 CAGGGCCTCAGGGGAGCAGAGG----GAGGGCCCTACTGCGAGATGAGGGAGGCCTCAGA 2063
 ||||| ||||| | |||| | | ||| ||||| |||||
 Db 1163 CAGGGCCTCAGGGGAGTCTCTGCTCCTCAAGCCCTGCTGGGAGTAAAGGGAGGCCTCAGG 1222

Qy 2064 GGACCCAGCACCCCTAGGA-----CACCAGCACCCCTGTCTGAGACTGAG--GCTGCC 2112
 | |||| | | |||| | | ||||| ||||| | | ||
 Db 1223 GAACCCAGGTCTCAGGATAGGGGGTCCACTCCAACCTGTCTGAGACTGAGGCGCCTCC 1282

Qy 2113 ACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGACCCAGG 2172
 ||| ||| |||| | |||| |||| | | ||||| ||||
 Db 1283 TCTTTCATCTCGGAATCAGGGATGGAGACTCAGTCAGCAGAGGGTGGGGCCCAAC 1342

Qy 2173 CCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGAATCCAGATC 2232
 |||| | | | | ||||| ||||| ||||| ||||| | ||||| |
 Db 1343 CCTGCCAGGATCAAGGAGAGGAAGAAGAGGGAGGACTCAGGGTACCTTTGAGTCCAGAAC 1402

Qy 2233 AGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTCC 2292
 | | |||| | ||||| ||||| |||| | ||||| | | |||||
 Db 1403 AATGGGGACCTTTGCCCTGGGAGGTCCAGTGCACAGTGGCCACCTGTAGCCCATGCTTGC 1462

Qy 2293 TGCATCTTTGAGGTGAC----AGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCA 2348
 |||| | | |||| | |||| | | ||||| ||| |||| | |||||
 Db 1463 TGCACCTTCTGGGTGACAAAGAGGAGAGGGCTGTGGTCTCAGAGCAGTGGTGAAGTCA 1522

Qy 2349 ACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATGAGGACTGG 2408
 ||||| |||| | || | | |||| | ||||| ||||| | |||
 Db 1523 GCAGAGGGAGGAGTCCAGCATCTGCAGGCCCAATGTGTGCCCCATTCATGAAGATTGG 1582

Qy 2409 GGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTTTTAGTAGC 2468
 |||| | | ||||| ||||| |||| | ||||| ||||| | | ||
 Db 1583 GGATA-CCTTGGCTCAGAAAGAAGGGACCCACAGAGTCTGGCTGTCCCCTGATTTTGC 1641

Qy 2469 TCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCAGG 2528
 || ||||| |||| |||| | |||| | |||| | |||| | ||||
 Db 1642 TCAGAGGGGACCAAATCAAGGATAGCCCTATGTGCCAACCTCATTTGTGCCACAGGAAAG 1701

Qy 2529 AAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGT 2588
 |||| | | ||||| ||||| |||| | |||| | |||| | ||||
 Db 1702 AAGTTGAAGAGCCCTCAGGGTGATGGGGTCTTGACAGTAAAGGGGAGCTATCTGCTCATCT 1761

Qy 2589 CAGGGAATTGGGGGTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGA 2648
 |||| | | ||||| |||| | | || | | || | | ||
 Db 1762 CAGGGGGTTTCAGGTTGAGGAATGGCAGGCCCATCACGATGAAGAGTAACCCACAGG-- 1819

Qy 2649 CAAGGCTATTGGAATCCACACCCCAAGAGGGTCAAGCCCTGGACACCTCA----- 2703
 || | | | | ||||| ||||| ||||| ||||| ||||| ||
 Db 1820 ---AGCCATAGAAACACTCACCCCAAGAGGGTCAACCTGGACACCCCATGTGG 1876

Qy 2704 ----CCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACC 2759
 ||||| || | | || | ||||| ||||| ||| ||||| |
 Db 1877 GGGTGACAGGATGTAGC-TCCATCTCATCTGTTTTCAGATCTCGGGGAGGTGAGGAAC 1935

Qy 2760 TCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGC 2819
 | |||| | || | ||||| |||| | ||||| |||| | |||||
 Db 1936 TTGTTCTCCGAGGATGACTCAGGTCAACACAGGGGCCCCCATCTGGTGGATAGACAGAGT 1995

Qy 2820 GGTCCCAGGATCTGCCATGCGTTCCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCA 2879
 |||||
 Db 1996 GGTCCCAGGATCTGTCTAGTAGTTCCGGTGAGGAACATGAGGGACGATTGAGGGCACCCCTT 2055

Qy 2880 GGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCCTGCTGTACACCCAG 2939
 |||||
 Db 2056 GGGCCAGAACACAGATGAGGACCTCACGGAAATCTGCCCTGCCCCCTGCTGTCACTCCAGA 2115

Qy 2940 GAGCATGGGCTGGGCCGTCTGCCGAGGTCTCTCC--GTTATCCTGGGATCATTGATGTCA 2997
 |||||
 Db 2116 GAGCATGGGCAGGGCTGTCTGCTGCAGTCCCCCCCCACTTACCTGGGATCATTGGTGTCA 2175

Qy 2998 GGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAG 3057
 |||||
 Db 2176 GGGATGGGGAGGTCTTTGTC-GAGGGGTCTGCACTCAGGTCAGTAGAGGGAGCGTCTTAG 2234

Qy 3058 GCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCC 3117
 |||||
 Db 2235 GCCCTGCCAGGAGACAAGGTAAGAACGAAGCAGGTTCTTCACCCAGGACACATGAATTCC 2294

Qy 3118 AATGAATTTTGATATCTCTTGCTGCCCTTCCCCA-AGGACCTAGGCACGTGTGGCCAGAT 3176
 |||||
 Db 2295 AATGCATTTTCAGCATCTCTTCCTGTCTTCCCCAAGAGGACCTGGGCACGTGTGGCCAGAT 2354

Qy 3177 GTTTGTCCCCTCCTGTCTTCCATTTCCTTATCATGGATGTGAACCTTGATTGATTTC 3236
 |||||
 Db 2355 GTGAGTCTCCTCATGTCTT---GTTCCCTATCAGGGATGTGAGCTCTTAATCTGAGTTTC 2411

Qy 3237 TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG 3296
 |||||
 Db 2412 TCAGGCCAGCAAAAGGGTGGGATCCAGGCCCTTGCCAGGAGAAAGGTGAGGGCCCTGTGTG 2471

Qy 3297 AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCCT 3356
 |||||
 Db 2472 AGCACAGAGGGGACCATTACCCCCAAGAGGGTGGAGACCTCACAGATTCCAGCCTACCCCT 2531

Qy 3357 CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT 3416
 |||||
 Db 2532 CCTGTTAGCACTGGGGGCCCTGAGGCTGTGCTTGCACTCTGCACCCTGAGGGCCCATGCAT 2591

Qy 3417 TCCTCTTCTGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA 3476
 |||||
 Db 2592 TCCTCTTCCAGGAGCTCCAGGAAACAGACACTGAGGCCTTGGTCTGAGGCCGTGCCCTCA 2651

Qy 3477 GGTCACAGAGCAGAGGATGCACAGGGT---GTGCCAGCAGTGAATGTTTGCCCTGAATG 3532
 |||||
 Db 2652 GGTCACAGAGCAGAGGAGATGCAGACGTCTAGTGCCAGCAGTGAACGTTTGCCCTGAATG 2711

Qy 3533 CACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCA-CC 3591
 |||||
 Db 2712 CACACTAATGGCCCCATCGCCCCAGAACATATGGGACTCCAGAGCACCTGGCCTCACCC 2771

Qy 3592 TCCCTACTGTCTAGTCTGTAGTAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTC 3651
 |||||
 Db 2772 TCTCTACTGTCTAGTCTGTAGTAATCGACCTCTGCTGGCCGGCTGTACCCTGAGGTGCCCTC 2831

Qy 3652 TCACCTTCTCTTCAGGTTTTCAGGGGACAGGCCAACCCAGAGGAC-----A 3698
 |||||
 Db 2832 TCACCTTTCTCTTCAGGTTTTCAGGGGACAGGCTGACCAGGATCACCAGGAAGCTCCAGA 2891

Qy 3699 GGATTCCCTGGAGGCCACAGAGGAGCACC-AAGGAGAAGATCTGTAAGTAGGCCTTTGTT 3757

Db	2892	GGATCCCCAGGAGGCCCTAGAGGAGCACCAAAGGAGAAGATCTGTAAGTAAGCCTTTGTT	2951
Qy	3758	AGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGC	3817
Db	2952	AGAGCCTCCAAGGTTTCAGTTTTTAGCTGAGGCTTCTCACATGCTCCCTCTCTCTCCAGGC	3011
Qy	3818	CTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTC	3877
Db	3012	CAGTGGGTCTCCATTGCCCAGCTCCTGCCCACACTCCTGCCTGTTGCGGTGACCAGAGTC	3071
Qy	3878	ATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAA	3937
Db	3072	GTCATGTCTCTTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGCCCTTGACACCCAA	3131
Qy	3938	CAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC-----C	3976
Db	3132	GAAGAGGCCCTGGGCCTGGTGGGTGTGCAGGCTGCCACTACTGAGGAGCAGGAGGCTGTG	3191
Qy	3977	TCCTCCTCCTCTCCTCTGGTCCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACA	4036
Db	3192	TCCTCCTCCTCTCCTCTGGTCCCAGGCACCCTGGGGGAGGTGCCTGCTGCTGGGTACCA	3251
Qy	4037	GATCCTCCCCAGAGTCTCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGA	4096
Db	3252	GGTCTCTCAAGAGTCTCTCAGGGAGCCTCCGCCATCCCCACTGCCATCGATTTCACCTCTA	3311
Qy	4097	CAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGT	4156
Db	3312	TGGAGGCAATCCATTAAGGGCTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTCCCCT	3371
Qy	4157	ATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTT	4216
Db	3372	GACCCAGAGTCTGTGTTCCGAGCAGCACTCAGTAAGAAGGTGGCTGACTTGATTCAATTTT	3431
Qy	4217	CTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCAAAAGGCAGAAATGCTGGAGAGTGTC	4276
Db	3432	CTGCTCCTCAAGTATTAAGTCAAGGAGCTGGTCAAAAGGCAGAAATGCTGGAGAGCGTC	3491
Qy	4277	ATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAG	4336
Db	3492	ATCAAAAATTACAAGCGCTGCTTTCTGAGATCTTCGGCAAAGCCTCCGAGTCCTTGCAG	3551
Qy	4337	CTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCAGCCACTCCTATGTCTTTGTC	4396
Db	3552	CTGGTCTTTGGCATTGACGTGAAGGAAGCGGACCCACCAGCAACACCTACACCTTTGTC	3611
Qy	4397	ACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTG---ATAATCAGATCATGCCCAAG	4453
Db	3612	ACCTGCCTGGG---ACTCCTATGATGGCCTGCTGGTTGATAATAATCAGATCATGCCCAAG	3669
Qy	4454	ACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAG	4513
Db	3670	ACGGGCCCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAAATGCGTCCCTGAG	3729
Qy	4514	GAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCC	4573
Db	3730	GAGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTC	3789
Qy	4574	TATGGGGAGCCCAAGGAGCTGCTCAGGAAAGTATTTGGTGCAGGAAAGTACCTGGAGTA-	4632

Db 3790 TGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAC TACCTGGAGTAC 3849

Qy 4633 CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCC TGTGGGGTCCAAGGGCCCTC 4692
 ||||| ||||| | ||||| ||||| |||||

Db 3850 CGGCAGGTGCCAGCAGTGATCCCATATGCTATGAGTTACTGTGGGGTCCAAGGGCACTC 3909

Qy 4693 GCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGC 4752
 |||| | ||||| || ||| | ||| ||| ||||| ||||| |

Db 3910 GCTGCT-----TGAAAGTACTGGAGCACGTGGTCAGGGTCAATGCAAGAGTTCTC 3959

Qy 4753 TTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCA 4812
 ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 3960 ATTTCTTACCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCA 4019

Qy 4813 TGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGT 4872
 |||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Db 4020 TGAGCTGCAGCCAGGGCCACTGCGAGGGGGGCTGGGCCAGTGCACCTTCCAGGGCTCCGT 4079

Qy 4873 CCAGCAGCTTCCCCTGCC--TCGTGTGACATGAGGCCCATTCCTTCACTC--TGAAAGAGAGC 4929
 |||| || ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||

Db 4080 CCAGTAGTTTCCCCTGCCCTTAATGTGACATGAGGCCCATTCCTTCTCTCTTTGAAGAGAGC 4139

Qy 4930 GGTCACTGTTCTCAGTAGAGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGT 4989
 |||| |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4140 AGTCAACATTCTTAGTAGTGGGTTTCTGTTCTATTGGATGACTTTGAGATTTGTCTTTGT 4199

Qy 4990 TCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATC 5049
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4200 TTCCTTTTGGGAATTGTTCAAATG-TTCTTTTAATGGGTGGTTGAATGAACTTCAGCATT 4258

Qy 5050 CAAGTTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGT 5107
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4259 CAAATTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGT 4318

Qy 5108 CTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAG 5165
 |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4319 CTTGTTTTTTATTTCAGATTGGGAAATCCATTCCATTTTGTGAATTGGGACATAGTTACAG 4378

Qy 5166 CAGTGGAAATAAGTACTTA-GAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAA 5224
 ||||| ||||| ||| | ||||| ||||| ||||| |

Db 4379 CAGTGGAAATAAGTATTCATTTAGAAATGTGAATGAGCAGTAAACTGATGACA----- 4431

Qy 5225 CTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAATTT 5284
 ||||| ||||| ||||| ||||| ||||| | ||| ||| |||

Db 4432 -TAAAGAAATTAAGAGATATTTAATTCTTGCTTATACTCAGTCTATTCGGTAAATTTTT 4490

Qy 5285 TTAAAGATATATGCATACCTGGATTTCCTTGCGCTCTTTGAGAATGTAAGAGAAATTA 5344
 || || | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4491 TTTAAAAAATGTGCATACCTGGATTTCCTTGCGCTCTTTGAGAATGTAAGACAAATTA 4550

Qy 5345 TCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTG 5404
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4551 TCTGAATAAATCATTCTCCCTGTTCACTGGCTCATTTATTCTCTATGCACTGAGCATTTG 4610

Qy 5405 CTTTTTGGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCAC 5464
 || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4611 CTCTGTGGGAAGGCCCTGGGTTAATAGTGGAGATGCTAAGGTAAGCCAGACTCACCCCTAC 4670

Qy 5465 CCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCT 5524
 ||| |||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 4671 CCACAGGGTAGTAAAGTCTAGGAGCAGCAGTCATATAATTAAGGTGGAGAGATGCCCTCT 4730

Qy 5525 AA 5526
||
Db 4731 AA 4732

RESULT 11

AAQ32351

ID AAQ32351 standard; DNA; 2419 BP.

XX

AC AAQ32351;

XX

DT 25-MAR-2003 (revised)

DT 22-APR-1993 (first entry)

XX

DE Antigen E gene.

XX

KW Stable; antigen; E; D; F; A; human; melanoma; cell line; MZ2-MEL;

KW cytolytic T cell; MEL3.1; open reading frame; homology; MAGE;

KW melanoma antigen; ss.

XX

OS Homo sapiens.

XX

PN WO9220356-A1.

XX

PD 26-NOV-1992.

XX

PF 22-MAY-1992; 92WO-US004354.

XX

PR 23-MAY-1991; 91US-00705702.

PR 09-JUL-1991; 91US-00728838.

PR 23-SEP-1991; 91US-00764364.

PR 12-DEC-1991; 91US-00807043.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Boon T, Van Der Bruggen P, Van Den Eynde B, Van Pel A, De Plaen E;

PI Lurquin C, Chomez P, Traversari C;

XX

DR WPI; 1992-415460/50.

XX

PT Nucleic acid mol. encoding a human tumour rejection antigen precursor -

PT useful as an immunostimulant in a vaccine for treating and preventing

PT cancers, also useful in diagnosis.

XX

PS Disclosure; Page 69-70; 142pp; English.

XX

CC This sequence encodes the stable antigen E. This antigen is expressed
CC along with antigens "D, F and A" by the human melanoma cell line MZ2-
CC MEL. These antigens are all recognised by cytolytic T cells. A subline of
CC MZ2-MEL is MEL3.1 which only expresses antigen E. This cell line was
CC chosen as a source for the isolation of this sequence. This sequence was
CC found to contain three exons. The open reading frame for antigen E was
CC contained within the first two exons. An ATG is located at position 66 of
CC exon 3 and is followed by an 828 base pair reading frame. The three exons
CC contain 65, 73 and 1551 base pairs. During the isolation of this sequence
CC two different but closely related cDNAs were also identified. These cDNAs,
CC when tested, did not transfer expression of antigen E, but they did show
CC substantial homology to the antigen E cDNA sequence. These new cDNAs
CC represent a new family of genes referred to as melanoma antigens (MAGE)
CC (see also AAQ32352-69). (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 U; 0 Other;

Query Match 42.6%; Score 2419; DB 2; Length 2419;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db       1  GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

QY      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61  ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

QY      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 3435
          |||
Db     121  CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 180

QY      3436 GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db     181  GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

QY      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db     241  CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

QY      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 3615
          |||
Db     301  CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 360

QY      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
          |||
Db     361  CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

QY      3676 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAA 3735
          |||
Db     421  GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAA 480

QY      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCCTCTCA 3795
          |||
Db     481  GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCCTCTCA 540

QY      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 3855
          |||
Db     541  CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 600

QY      3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
          |||
Db     601  GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

QY      3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
          |||
Db     661  TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

QY      3976 CTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCACCTGCTGGGTCAAC 4035
          |||
Db     721  CTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCACCTGCTGGGTCAAC 780

QY      4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 4095
          |||
```

Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	4635
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	1380
Qy	4636	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	4695
Db	1381	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	1440
Qy	4696	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	4755
Db	1441	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	1500
Qy	4756	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	4815
Db	1501	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	1560
Qy	4816	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	4875
Db	1561	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	1620
Qy	4876	GCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	4935
Db	1621	GCAGCTTCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	1680
Qy	4936	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	4995
Db	1681	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	1740

Qy	4996	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT	5055
Db	1741	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT	1800
Qy	5056	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	5115
Db	1801	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	1860
Qy	5116	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA	5175
Db	1861	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA	1920
Qy	5176	AGTACTTAGAAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	5235
Db	1921	AGTACTTAGAAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	1980
Qy	5236	AAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	5295
Db	1981	AAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	2040
Qy	5296	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	5355
Db	2041	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	2100
Qy	5356	AATTCTTCCTGTTCACCTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGAAG	5415
Db	2101	AATTCTTCCTGTTCACCTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGAAG	2160
Qy	5416	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	5475
Db	2161	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	2220
Qy	5476	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	5535
Db	2221	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	2280
Qy	5536	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC	5595
Db	2281	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC	2340
Qy	5596	CCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	5655
Db	2341	CCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	2400
Qy	5656	AATGATCTTGGGTGGATCC	5674
Db	2401	AATGATCTTGGGTGGATCC	2419

RESULT 12

AAQ72476

ID AAQ72476 standard; DNA; 2419 BP.

XX

AC AAQ72476;

XX

DT 25-MAR-2003 (revised)

DT 21-JUN-1995 (first entry)

XX

DE Tumour rejection antigen E encoding DNA.

XX

KW Tumour rejection antigen E; melanoma antigen-3; MAGE-3; cancer;
KW cytolytic T cells; antigen D; human leucocyte antigen; ss.
XX
OS Homo sapiens.
XX
PN WO9423031-A1.
XX
PD 13-OCT-1994.
XX
PF 17-MAR-1994; 94WO-US002877.
XX
PR 26-MAR-1993; 93US-00037230.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Gaugler B, Van Den Eynde B, Boon-Falleur T, Van Der Bruggen P;
XX
DR WPI; 1994-333192/41.
XX
PT New tumour rejection antigen precursor MAGE3 - useful in treatment and
PT diagnosis of cancer.
XX
PS Disclosure; Page 58; 105pp; English.
XX
CC AAQ72476 encodes tumour rejection antigen E, another sequence AAQ72470
CC encodes melanoma antigen-3 (MAGE-3) a tumour rejection antigen precursor.
CC Melanomas characterised by the expression of MAGE-3 can be detected, or
CC monitored, by contacting a test sample with an agent that can recognise
CC MAGE-3. The melanoma can be treated by the administration of cytolytic T
CC cells specific for the complex of antigen D (the mature rejection antigen
CC derived from MAGE-3) and a human leucocyte antigen (esp. HLA-A1).
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 U; 0 Other;

Db 301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCCTGTAGAAT 360

Qy 3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
 |||

Db 361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy 3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
 |||

Db 421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy 3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
 |||

Db 481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy 3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 3855
 |||

Db 541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 600

Qy 3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
 |||

Db 601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy 3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
 |||

Db 661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy 3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035
 |||

Db 721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780

Qy 4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 4095
 |||

Db 781 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 840

Qy 4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 4155
 |||

Db 841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 900

Qy 4156 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT 4215
 |||

Db 901 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT 960

Qy 4216 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 4275
 |||

Db 961 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 1020

Qy 4276 CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 4335
 |||

Db 1021 CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 1080

Qy 4336 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTTCCTTGT 4395
 |||

Db 1081 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTTCCTTGT 1140

Qy 4396 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 4455
 |||

Db 1141 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 1200

Qy 4456 AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 4515
 |||

Db 1201 AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 1260

Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	4635
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	1380
Qy	4636	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	4695
Db	1381	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	1440
Qy	4696	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	4755
Db	1441	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	1500
Qy	4756	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	4815
Db	1501	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	1560
Qy	4816	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	4875
Db	1561	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	1620
Qy	4876	GCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	4935
Db	1621	GCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	1680
Qy	4936	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	4995
Db	1681	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	1740
Qy	4996	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTT	5055
Db	1741	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTT	1800
Qy	5056	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	5115
Db	1801	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	1860
Qy	5116	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGGAATA	5175
Db	1861	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGGAATA	1920
Qy	5176	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	5235
Db	1921	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	1980
Qy	5236	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	5295
Db	1981	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	2040
Qy	5296	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	5355
Db	2041	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	2100
Qy	5356	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGAAG	5415
Db	2101	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGAAG	2160

```

Qy      5416 GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 5475
          |||
Db      2161 GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 2220

Qy      5476 TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG 5535
          |||
Db      2221 TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG 2280

Qy      5536 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC 5595
          |||
Db      2281 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC 2340

Qy      5596 CCTGAGCTGGGGCATTCTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGT 5655
          |||
Db      2341 CCTGAGCTGGGGCATTCTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGT 2400

Qy      5656 AATGATCTTGGGTGGATCC 5674
          |||
Db      2401 AATGATCTTGGGTGGATCC 2419

```

RESULT 13

AAX84112

ID AAX84112 standard; DNA; 2419 BP.

XX

AC AAX84112;

XX

DT 08-SEP-1999 (first entry)

XX

DE Antigen E coding sequence.

XX

KW Tumour rejection antigen; vaccine; cancer; antigen E; ss.

XX

OS Homo sapiens.

XX

PN US5925729-A.

XX

PD 20-JUL-1999.

XX

PF 02-MAY-1994; 94US-00142368.

XX

PR 23-MAY-1991; 91US-00705702.

PR 09-JUL-1991; 91US-00728838.

PR 23-SEP-1991; 91US-00764365.

PR 12-DEC-1991; 91US-00807043.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Van Der Bruggen P, Traversari C, Lurquin C, Boon T, De Plaen E;

PI Van Pel A, Chomez P, Van Den Eynde B;

XX

DR WPI; 1999-418294/35.

XX

PT New tumour rejection antigen is useful as a vaccine against cancerous diseases.

XX

PS Disclosure; Col 37-40; 58pp; English.

XX

CC This sequence represents the antigen E coding sequence. The invention relates to a tumour rejection antigen sequence that is useful as a tumour rejection antigen for vaccination against cancerous conditions

XX

SQL Sequence 2419 BP; 562 A; 581 C; 677 G; 599 T; 0 U; 0 Other;

Query Match 42.6%; Score 2419; DB 2; Length 2419;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db      1   GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61   ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 3435
          |||
Db      121  CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181  GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241  CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          |||
Db      301  CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTCAGGTTTTTCAG 3675
          |||
Db      361  CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
          |||
Db      421  GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCCTCAGCTGAGGCCTCTCA 3795
          |||
Db      481  GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 3855
          |||
Db      541  CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 600

Qy      3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
          |||
Db      601  GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy      3916 TGAGGAAGCCCTTGAGGCCCCAACAAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
          |||
Db      661  TGAGGAAGCCCTTGAGGCCCCAACAAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy      3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035
          |||
Db      721  CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780

Qy      4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 4095
          |||
```

Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	4635
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	1380
Qy	4636	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGTCCAAGGGCCCTCGCT	4695
Db	1381	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGTCCAAGGGCCCTCGCT	1440
Qy	4696	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	4755
Db	1441	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	1500
Qy	4756	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	4815
Db	1501	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	1560
Qy	4816	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	4875
Db	1561	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	1620
Qy	4876	GCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	4935
Db	1621	GCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	1680
Qy	4936	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	4995
Db	1681	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	1740

Qy	4996	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT	5055
Db	1741	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGTT	1800
Qy	5056	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	5115
Db	1801	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	1860
Qy	5116	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGAATA	5175
Db	1861	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGAATA	1920
Qy	5176	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	5235
Db	1921	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	1980
Qy	5236	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	5295
Db	1981	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	2040
Qy	5296	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	5355
Db	2041	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	2100
Qy	5356	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGGAAG	5415
Db	2101	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGGAAG	2160
Qy	5416	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	5475
Db	2161	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	2220
Qy	5476	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	5535
Db	2221	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	2280
Qy	5536	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC	5595
Db	2281	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC	2340
Qy	5596	CCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	5655
Db	2341	CCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	2400
Qy	5656	AATGATCTTGGGTGGATCC	5674
Db	2401	AATGATCTTGGGTGGATCC	2419

RESULT 14

AAT05086

ID AAT05086 standard; DNA; 2419 BP.

XX

AC AAT05086;

XX

DT 25-MAR-2003 (revised)

DT 26-FEB-1996 (first entry)

XX

DE MZ2-MEL antigen E precursor gene.

XX

KW Melanoma; MZ2-MEL; tumour rejection antigen; cancer; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9523874-A1.
 XX
 PD 08-SEP-1995.
 XX
 PF 23-FEB-1995; 95WO-US002203.
 XX
 PR 01-MAR-1994; 94US-00204727.
 PR 10-MAR-1994; 94US-00209172.
 PR 01-SEP-1994; 94US-00299849.
 PR 30-NOV-1994; 94US-00346774.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI De Plaen E, Boon-Falleur T, Lethe B, Szikora J, De Smet C;
 PI Chomez P, Gaugler B, Van Den Eynde B, Brasseur F, Patard J;
 PI Weynants P, Marchand M, Van Der Bruggen P;
 XX
 DR WPI; 1995-320586/41.
 XX
 PT Determn. of cancerous condition(s) - using a nucleic acid as a primer to
 PT determine expression of a MAGE tumour rejection antigen precursor.
 XX
 PS Example 20; Page 69-70; 121pp; English.
 XX
 CC A gene sequence (AAT05086) hybridizes with a 2.4 kb fragment from human
 CC melanoma cell line MZ2-MEL but not with E- antigen loss variants of MZ2-
 CC MEL. This E precursor antigen gene sequence was obtd. from a cosmid
 CC derived from DNA of the E+ subclone MZ2-MEL 43. (Updated on 25-MAR-2003
 CC to correct PI field.)
 XX
 SQ Sequence 2419 BP; 560 A; 581 C; 677 G; 601 T; 0 U; 0 Other;

Query Match 42.6%; Score 2415.8; DB 2; Length 2419;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2417; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60
 Qy 3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120
 Qy 3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTCCTGGAGCTCCA 3435
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTCCTGGAGCTCCA 180
 Qy 3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240
 Qy 3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300
 Qy 3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615

Db	301		CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCTAGTCCCTGTAGAAAT	360
Qy	3616		CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	3675
Db	361		CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	420
Qy	3676		GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAA	3735
Db	421		GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAA	480
Qy	3736		GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	3795
Db	481		GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	540
Qy	3796		CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	3855
Db	541		CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	600
Qy	3856		GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601		GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916		TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661		TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976		CTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721		CTCCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036		AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781		AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096		ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841		ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156		TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901		TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216		TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961		TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276		CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021		CATCATTAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336		GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081		GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396		CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141		CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456		AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515

Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	4635
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	1380
Qy	4636	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	4695
Db	1381	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	1440
Qy	4696	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	4755
Db	1441	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTT	1500
Qy	4756	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	4815
Db	1501	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	1560
Qy	4816	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCAGGGCCGCGTCCA	4875
Db	1561	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCAGGGCCGCGTCCA	1620
Qy	4876	GCAGCTTCCCTGCGTCGTGTGACATGAGGCCCATTCCTTCACTCTGAAGAGAGCGGTCAG	4935
Db	1621	GCAGCTTCCCTGCGTCGTGTGACATGAGGCCCATTCCTTCACTCTGAAGAGAGCGGTCAG	1680
Qy	4936	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	4995
Db	1681	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	1740
Qy	4996	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTT	5055
Db	1741	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTT	1800
Qy	5056	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	5115
Db	1801	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTT	1860
Qy	5116	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA	5175
Db	1861	TTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA	1920
Qy	5176	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	5235
Db	1921	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	1980
Qy	5236	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	5295
Db	1981	AAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	2040
Qy	5296	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	5355
Db	2041	TGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAG	2100
Qy	5356	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGAAG	5415
Db	2101	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGAAG	2160

Qy 5416 GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 5475
 |||
 Db 2161 GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG 2220

Qy 5476 TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG 5535
 |||
 Db 2221 TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG 2280

Qy 5536 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC 5595
 |||
 Db 2281 GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGC 2340

Qy 5596 CCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT 5655
 |||
 Db 2341 CCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT 2400

Qy 5656 AATGATCTTGGGTGGATCC 5674
 |||
 Db 2401 AATGATCTTGGGTGGATCC 2419

RESULT 15

AAQ72472

ID AAQ72472 standard; DNA; 2420 BP.

XX

AC AAQ72472;

XX

DT 25-MAR-2003 (revised)

DT 21-JUN-1995 (first entry)

XX

DE Tumour rejection antigen E precursor gene DNA.

XX

KW Tumour antigen rejection precursor E; melanoma antigen-3; MAGE-3; cancer;
 KW cytolytic T cells; antigen D; human leucocyte antigen; ss.

XX

OS Homo sapiens.

XX

PN WO9423031-A1.

XX

PD 13-OCT-1994.

XX

PF 17-MAR-1994; 94WO-US002877.

XX

PR 26-MAR-1993; 93US-00037230.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Gaugler B, Van Den Eynde B, Boon-Falleur T, Van Der Bruggen P;

XX

DR WPI; 1994-333192/41.

XX

PT New tumour rejection antigen precursor MAGE3 - useful in treatment and
 PT diagnosis of cancer.

XX

PS Example 20; Page 28; 105pp; English.

XX

CC AAQ72472 is the tumour rejection antigen E precursor gene, another gene

CC AAQ72470 encodes melanoma antigen-3 (MAGE-3) also a tumour rejection

CC antigen precursor. Melanomas characterised by the expression of MAGE-3

CC can be detected, or monitored, by contacting a test sample with an agent

CC that can recognise MAGE-3. The melanoma can be treated by the
CC administration of cytolytic T cells specific for the complex of antigen D
CC (the mature rejection antigen derived from MAGE-3) and a human leucocyte
CC antigen (esp. HLA-A1). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 2420 BP; 562 A; 582 C; 677 G; 599 T; 0 U; 0 Other;

Query Match 42.4%; Score 2408; DB 2; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  ACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGGAGCTCCA 3435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCCTTCAGGTTTTTCAG 3675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCTCCTGCCCCACACTCCT 3855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCAGCTCCTGCCCCACACTCCT 600

Qy      3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy      3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy      3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTGGAGGAGGTGCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680

Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	1740
Qy	4995	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	5054
Db	1741	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAA	5174
Db	1861	TTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAA	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	2160
Qy	5415	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG	5534
Db	2221	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG	2280
Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGCAATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGCAATG	2340
Qy	5595	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400
Qy	5655	TAATGATCTTGGGTGGATCC	5674
Db	2401	TAATGATCTTGGGTGGATCC	2420

Search completed: August 25, 2006, 10:01:56
Job time : 3217 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e- 8.rnpbm.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
--	--	--	--	---

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-8.rnpbm.

[start](#)

[Go Back to previous pag](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 12:01:51 ; Search time 6169 Seconds
(without alignments)
11301.677 Million cell updates/sec

Title: US-08-819-669E-8
Perfect score: 5674
Sequence: 1 CCCGGGGCACCCTGGCATC.....TAATGATCTGGGTGGATCC 5674

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query		DB	ID	Description
			Match	Length			
c	1	5567.8	98.1	259903	10	US-10-756-149-3550	Sequence 3550, Ap
	2	2513.6	44.3	4895	6	US-10-102-524-1696	Sequence 1696, Ap
	3	2513.6	44.3	4895	9	US-10-482-029-147	Sequence 147, App
	4	2422.8	42.7	4741	9	US-10-482-029-87	Sequence 87, Appl
	5	2408	42.4	2420	7	US-10-117-937-81	Sequence 81, Appl
	6	2408	42.4	2420	9	US-10-741-466-5	Sequence 5, Appli
	7	2408	42.4	2420	9	US-10-657-022-81	Sequence 81, Appl
	8	2408	42.4	2420	9	US-10-807-308-17	Sequence 17, Appl
	9	2408	42.4	2420	9	US-10-866-484-5	Sequence 5, Appli
	10	2408	42.4	2420	9	US-10-482-029-91	Sequence 91, Appl
	11	2408	42.4	2420	10	US-10-871-708-14	Sequence 14, Appl
	12	2408	42.4	2420	13	US-11-067-064-81	Sequence 81, Appl
	13	2408	42.4	2420	13	US-11-067-159-81	Sequence 81, Appl
	14	2408	42.4	2420	16	US-11-155-288-25	Sequence 25, Appl
	15	2404.8	42.4	2420	6	US-10-093-766-41	Sequence 41, Appl
	16	2404.8	42.4	2420	6	US-10-116-802-250	Sequence 250, App
c	17	2390.4	42.1	2408	6	US-10-027-632-111713	Sequence 111713,
c	18	2390.4	42.1	2408	6	US-10-027-632-111714	Sequence 111714,
c	19	2390.4	42.1	2408	7	US-10-027-632-111713	Sequence 111713,
c	20	2390.4	42.1	2408	7	US-10-027-632-111714	Sequence 111714,
c	21	2307.6	40.7	302250	3	US-09-962-832-154	Sequence 154, App
c	22	2307.6	40.7	302250	10	US-10-843-641A-6040	Sequence 6040, Ap
	23	2306	40.6	302250	3	US-09-962-832-154	Sequence 154, App
	24	2306	40.6	302250	10	US-10-843-641A-6040	Sequence 6040, Ap
	25	2117.8	37.3	4559	7	US-10-117-937-82	Sequence 82, Appl
	26	2117.8	37.3	4559	9	US-10-657-022-82	Sequence 82, Appl
	27	2117.8	37.3	4559	13	US-11-067-064-82	Sequence 82, Appl
	28	2117.8	37.3	4559	13	US-11-067-159-82	Sequence 82, Appl
	29	1945	34.3	4523	8	US-10-444-683-43	Sequence 43, Appl
	30	1765.8	31.1	4204	6	US-10-116-802-229	Sequence 229, App
	31	1762.6	31.1	4204	3	US-09-954-456-747	Sequence 747, App
	32	1762.6	31.1	4204	3	US-09-784-199-1	Sequence 1, Appli
	33	1762.6	31.1	4204	3	US-09-860-840-1	Sequence 1, Appli
	34	1762.6	31.1	4204	3	US-09-849-602-14	Sequence 14, Appl
	35	1762.6	31.1	4204	7	US-10-170-832-1	Sequence 1, Appli
	36	1762.6	31.1	4204	7	US-10-117-937-83	Sequence 83, Appl
	37	1762.6	31.1	4204	8	US-10-444-683-1	Sequence 1, Appli
	38	1762.6	31.1	4204	9	US-10-657-022-83	Sequence 83, Appl
	39	1762.6	31.1	4204	9	US-10-482-029-89	Sequence 89, Appl
	40	1762.6	31.1	4204	10	US-10-843-641A-3774	Sequence 3774, Ap
	41	1762.6	31.1	4204	10	US-10-871-708-15	Sequence 15, Appl
	42	1762.6	31.1	4204	13	US-11-067-064-83	Sequence 83, Appl
	43	1762.6	31.1	4204	13	US-11-067-159-83	Sequence 83, Appl
	44	1762.6	31.1	4204	16	US-11-155-288-26	Sequence 26, Appl
	45	1677	29.6	3871	9	US-10-482-029-93	Sequence 93, Appl

ALIGNMENTS

RESULT 1

US-10-756-149-3550/c
; Sequence 3550, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS A
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3550
; LENGTH: 259903
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-3550

Query Match 98.1%; Score 5567.8; DB 10; Length 259903;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 5655; Conservative 0; Mismatches 17; Indels 7; Gaps 7;

```

Qy      1  CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
      |||
Db 112112 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 112053

Qy      61  ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120
      |||
Db 112052 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 111993

Qy     121  CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 180
      |||
Db 111992 CTCTCAACCCAGGGAAGCCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG 111933

Qy     181  TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 240
      |||
Db 111932 TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG 111873

Qy     241  CCCA-GCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCC 299
      |||
Db 111872 CCCAGGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCC 111813

Qy     300  CAGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTT 359
      |||
Db 111812 CAGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTT 111753

Qy     360  CTCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGA 419
      |||
Db 111752 CTCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCTGAAGTCAG 111693

Qy     420  GCTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACA 479
      |||
Db 111692 AGCTCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACA 111633

Qy     480  TCATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAA 539
      |||
Db 111632 TCATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAA 111573

Qy     540  CCCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCC 599
      |||

```

Db	111572	CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCCTCTTCATTGTCATTCCAACCCCC	111513
Qy	600	ACCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCC	659
Db	111512	ACCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCC	111453
Qy	660	TCACCCCCACCCCCACCCCCACGCCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCC	719
Db	111452	TCACCCCCACCCCCACCCCCACGCCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCC	111393
Qy	720	GCCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAG	779
Db	111392	GCCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAG	111333
Qy	780	AGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAG	839
Db	111332	AGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAG	111273
Qy	840	GCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAAT	899
Db	111272	GCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCGCCACTCCAAAT	111213
Qy	900	AGAGAGCCCCAAATATTCCAGCCCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAG	959
Db	111212	AGAGAGCCCCAAATATTCCAGCGCCGCCCTTGCTGCCAGCCCTGGCCCACCCGCGGGAAG	111153
Qy	960	ACGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTT	1019
Db	111152	ACGTCTCAGCCTGGGCTGCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTT	111093
Qy	1020	CTTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAG	1079
Db	111092	CTTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAG	111033
Qy	1080	GGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCC	1139
Db	111032	GGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCC	110973
Qy	1140	CCCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAAC	1199
Db	110972	CCCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCCCACCCAAC	110913
Qy	1200	CCCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCAC	1259
Db	110912	CCCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCACCTGACCAC	110853
Qy	1260	CACCCTCCAGCCCCAGCACCCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAA	1319
Db	110852	CACCCTCCAGCCCCAGCACCCAGCCCCAACCCCTTCTGCCACCTCACCCTCACTGCCCCAA	110793
Qy	1320	CCCCACCCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTTCTGGCAGAATC	1379
Db	110792	CCCCACCCTCATCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTTCTGGCAGAATC	110733
Qy	1380	CGGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGAC	1439
Db	110732	CGGTTTGCCCCTGCTCTCAACCCAGGGAAGCCCTGGATGGCCCGATGTGAAACCACTGAC	110673
Qy	1440	TTGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGA	1499
Db	110672	TTGAACCTCACAGATCTGAGAGAAGCCAGGTTCAATTAATGGTTCTGAGGGGCGGCTTGA	110613

Qy	1500	GATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAG	1559
Db	110612	GATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAG	110553
Qy	1560	GACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCT	1619
Db	110552	GACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCT	110493
Qy	1620	GCCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCCGTC	1679
Db	110492	GCCAGCCCTGGACCACCCGCCAGGACAGATGTCTCAGCTGGACCACCCCCGTC	110433
Qy	1680	CCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGT	1739
Db	110432	CCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGT	110373
Qy	1740	TGGTCAGGAGA-GGCAGGGCCCAGGCATCAAGGTCCA-GCATCCGCCCGGCATTAGGGTC	1797
Db	110372	TGGTCAGGAGAGGGCAGGGCCCAGGCATCAAGGTCCAGGCATCCGCCCGGCATTAGGGTC	110313
Qy	1798	AGGACCCTGGGAGGGAAGTGGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCC	1857
Db	110312	AGGACCCTGGGAGGGAAGTGGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCC	110253
Qy	1858	ACCCCACTCACATTCCCACATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTG	1917
Db	110252	ACCCCACTCACATTCCCACATACCTACCCCTACCCCAACCTCATCTTGTCAGAATCCCTG	110193
Qy	1918	CTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCAT	1977
Db	110192	CTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCAT	110133
Qy	1978	CCAGGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCC	2037
Db	110132	CCAGGG-CTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCC	110074
Qy	2038	TACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCT	2097
Db	110073	TACTGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCTTAGGACACCGCACCCCTGTCT	110014
Qy	2098	GAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATT-GCAT	2156
Db	110013	GAGACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTAGCAT	109954
Qy	2157	GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGA	2216
Db	109953	GGGGGTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGA	109894
Qy	2217	CCTTGGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACA	2276
Db	109893	CCTTGGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACA	109834
Qy	2277	TATGGCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGG	2336
Db	109833	TATGGCCCATATTTCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGG	109774
Qy	2337	GGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTT	2396
Db	109773	GGCCTCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTT	109714

Qy	2397	CATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCC	2456
Db	109713	CATGAGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCC	109654
Qy	2457	CCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGT	2516
Db	109653	CCTTTTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGT	109594
Qy	2517	ACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGAT	2576
Db	109593	ACCACAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGAT	109534
Qy	2577	GTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGAT	2636
Db	109533	GTCTACTCATGTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGAT	109474
Qy	2637	GAGTGAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTCAGCCCTGGA	2696
Db	109473	GAGTGAGACAGACAAGGCTATTGGAATCCTCACCCCAGAACCAAAGGGGTCAGCCCTGGA	109414
Qy	2697	CACCTCACCCAGGATGTGGCTTCTTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGG	2756
Db	109413	CACCTCACCCAGGATGTGGCTTC-TTTTTCACCTCTGTTTCCAGATCTGGGGCAGGTGAGG	109355
Qy	2757	ACCTCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAG	2816
Db	109354	ACCTCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAG	109295
Qy	2817	AGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACC	2876
Db	109294	AGCGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACC	109235
Qy	2877	CCAGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCC	2936
Db	109234	CCAGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCC	109175
Qy	2937	AGAGAGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTC	2996
Db	109174	AGAGAGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTC	109115
Qy	2997	AGGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCA	3056
Db	109114	AGGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCA	109055
Qy	3057	GGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTC	3116
Db	109054	GGCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTC	108995
Qy	3117	CAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGAT	3176
Db	108994	CAATGAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGAT	108935
Qy	3177	GTTTGTCCCCCTCTGTCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGTGGATTTC	3236
Db	108934	GTTTGTCCCCCTCTGTCTTCCATTCCCTTATCATGGATGTGAACCTTGATTGTGGATTTC	108875
Qy	3237	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	3296
Db	108874	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	108815
Qy	3297	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCT	3356

Db	108814		AGAACAGAGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCT	108755
Qy	3357		CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT	3416
Db	108754		CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT	108695
Qy	3417		TCCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	3476
Db	108694		TCCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	108635
Qy	3477		GGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACA	3536
Db	108634		GGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACA	108575
Qy	3537		CCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCT	3596
Db	108574		CCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCT	108515
Qy	3597		ACTGTCAGTCCGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACT	3656
Db	108514		ACTGTCAGTCCGTAGAAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACT	108455
Qy	3657		TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCAC	3716
Db	108454		TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCAC	108395
Qy	3717		AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT	3776
Db	108394		AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT	108335
Qy	3777		TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC	3836
Db	108334		TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCC	108275
Qy	3837		AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	108274		AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	108215
Qy	3897		GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Db	108214		GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	108155
Qy	3957		TGTGTGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGG	4016
Db	108154		TGTGTGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCTGGGCACCCTGGAGGAGG	108095
Qy	4017		TGCCCCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCA	4076
Db	108094		TGCCCCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCA	108035
Qy	4077		CTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGG	4136
Db	108034		CTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGG	107975
Qy	4137		AGGGGCCAAGCACCTCTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGG	4196
Db	107974		AGGGGCCAAGCACCTCTGTATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGG	107915
Qy	4197		TGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG	4256

Db 107914 TGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG 107855

Qy 4257 CAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCA 4316
 |||

Db 107854 CAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCA 107795

Qy 4317 AAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCG 4376
 |||

Db 107794 AAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCG 107735

Qy 4377 GCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATA 4436
 |||

Db 107734 GCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATA 107675

Qy 4437 ATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGG 4496
 |||

Db 107674 ATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGG 107615

Qy 4497 GCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATG 4556
 |||

Db 107614 GCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATG 107555

Qy 4557 GGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCAAGATTTGGTGCAGG 4616
 |||

Db 107554 GGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCAAGATTTGGTGCAGG 107495

Qy 4617 AAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGACGCTATGAGTTCCTGT 4675
 |||

Db 107494 AAAAGTACCTGGAGTACCGCAGGTGCCGGACAGTGATCCCGACGCTATGAGTTCCTGT 107435

Qy 4676 GGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGG 4735
 |||

Db 107434 GGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGG 107375

Qy 4736 TCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGG 4795
 |||

Db 107374 TCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGG 107315

Qy 4796 AAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGC 4855
 |||

Db 107314 AAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGC 107255

Qy 4856 ACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTC 4915
 |||

Db 107254 ACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTC 107195

Qy 4916 ACTCTGAAGAGAGCGGTCAAGTTCAGTAGTAGGTTCTGTTCTATTGGGTGACTTGG 4975
 |||

Db 107194 ACTCTGAAGAGAGCGGTCAAGTTCAGTAGTAGGTTCTGTTCTATTGGGTGACTTGG 107135

Qy 4976 AGATTTATCTTTGTTCTTTTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAA 5035
 |||

Db 107134 AGATTTATCTTTGTTCTTTTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAA 107075

Qy 5036 TGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTT 5095
 |||

Db 107074 TGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTT 107015

Qy 5096 AAGGGTAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG 5155
 |||

Db 107014 AAGGGTAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG 106955

Qy 5156 ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGA 5215
 |||
 Db 106954 ATAATAACAGCAGTGGAAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGA 106895

Qy 5216 GATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCT 5275
 |||
 Db 106894 GATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCT 106835

Qy 5276 GTAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGA 5335
 |||
 Db 106834 GTAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGA 106775

Qy 5336 GAAATTAAATCTGAATAAAGAATTCTTCCTGTTTCACTGGCTCTTTTCTTCTCCATGCACT 5395
 |||
 Db 106774 GAAATTAAATCTGAATAAAGAATTCTTCCTGTTTCACTGGCTCTTTTCTTCTCCATGCACT 106715

Qy 5396 GAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACT 5455
 |||
 Db 106714 GAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACT 106655

Qy 5456 CATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAG 5515
 |||
 Db 106654 CATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAG 106595

Qy 5516 ATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGA 5575
 |||
 Db 106594 ATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGA 106535

Qy 5576 GAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTC 5635
 |||
 Db 106534 GAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTTGGGCTTTGGGAACTGCAGTTC 106475

Qy 5636 CTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
 |||
 Db 106474 CTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 106436

RESULT 2

US-10-102-524-1696

; Sequence 1696, Application US/10102524

; Publication No. US20030109434A1

; GENERAL INFORMATION:

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Gaiger, Alexander

; APPLICANT: Gordon, Brian

; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER

; FILE REFERENCE: 210121.572

; CURRENT APPLICATION NUMBER: US/10/102,524

; CURRENT FILING DATE: 2002-03-19

; NUMBER OF SEQ ID NOS: 1863

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 1696

; LENGTH: 4895

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-102-524-1696

Query Match 44.3%; Score 2513.6; DB 6; Length 4895;
Best Local Similarity 79.9%; Pred. No. 0;
Matches 3415; Conservative 0; Mismatches 694; Indels 165; Gaps 32;

Qy	1478	ATGGTTC TGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGGTTTTTAGGCTCTGTGAGGAG	1537
Db	607	ATAGTCCTGAGGGGCCAGTTGAGATCGGCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAG	666
Qy	1538	GCAAGGTGAGATGCTGAGGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAA	1597
Db	667	GCAAGGTGAGACTCTGAGGAAGGACTGAGGAGGCCCCACCCAAGATAGA-GGAACCCAA	725
Qy	1598	ATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAG	1657
Db	726	ATAATCCAGCCCACGTCTCTGCTGCCAGTCTTGGACCACCCGG---GGGAAGACTTCTCA-	781
Qy	1658	CTGGACCACCCCCGTCCTCCGCTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATA	1717
Db	782	---GGCTAGGCCATCCCAGCTCCCACTGCCACTAAAGCTACAGGGGACTCTAGAGTCA--	836
Qy	1718	GCTTATGTGACCGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGC	1777
Db	837	-----AGAGCTTGGTGTGCCCAAGGCAGGGCCAGG	866
Qy	1778	ATCCGCCCGGCATTAGGGTCAGGACCCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCT	1837
Db	867	CTCTGCC TGGCATCGGGGT CAGGACCTTGAGAGGGAAGTGAAGGCGCTACACCCCAACC	926
Qy	1838	GTCTCTCATCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTTACCCCAACC	1897
Db	927	CATCCGCATTC-----CAACATGCCCAGCCCCATCCCAACTCCGTTTTCAGAA	976
Qy	1898	TCATCTTGTCAGAATCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCAC	1957
Db	977	TCCATTTTT---TCCCCTGCAGTCAACCCCGGGAAGACCTGGGAATGGT---CAGGCAC	1029
Qy	1958	TCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAACAG	2010
Db	1030	TCGGATCTTGACATCCACATCGAGGGCTGAAGGAGGGAGAGAGTTTGGTATCATGAGCAG	1089
Qy	2011	GGCCTCAGGGGAGCAGAGGGAG-----GGCCCTACTGCGAGATGAGGGAGGCCTCAGAG	2064
Db	1090	AGCCTCAGGGTAGCAGAGGGAGGACCCTGGCCCTCCTGGGAGATGAGGAAGGCCTCAGGA	1149
Qy	2065	GACCCAGCACCC-----TAGGACACCGCACCCCTGTCTGAGACTGAG--GCTGCCA	2113
Db	1150	GACCCAGCACCCCAAGGCAGGGAGCCACCCACCCCTGTCTGAGAATGAGGTGCCTCTCT	1209
Qy	2114	CTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGA--CCCAG	2171
Db	1210	CCTTTAGCCTCAGGAATCCAAGGGATGGCAACTCAGGTCAGCAGAGGGGTGGGTTCAG	1269
Qy	2172	GCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGAATCCAGAT	2231
Db	1270	CCCTTCCAGGATCAAGGAAAGGAAGACGAGGGAGGATTGAGGGGCGCTTGCATTCCAGAT	1329
Qy	2232	CAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTT	2291
Db	1330	CAGTGGAGACCTGGGCCCTGGGAGGTCTGGGCAAGGTAGCCACCTGTAGCTCATACTTC	1389
Qy	2292	CTGCATCTTTGAGGT---GACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTC	2347

Db	1390	CTGCATCTTCGAGGTCACAGAGAGGAGAGGGCTATGGTCTGAGGGGTGGTACTTCAGGTC	1449
Qy	2348	AACAGAGGGAGGAGTTCCAGGATCCATATGGCCCCAAGATGTGCC-CCCTTCATGAGGACT	2406
Db	1450	CGCAGAGGGAGGAGTCCCAGGATCTACAGGACCCAAGGTGTGCCACACTTCACGAGGAAT	1509
Qy	2407	GGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCCTTTTAGTA	2466
Db	1510	GGGGATACCTGTGGCTCAGAAAGACGGGACCCACAGAGTCTGGCTGTCCCCTGTCTTA	1569
Qy	2467	GCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCA	2526
Db	1570	GCTCAGGGGGGACCAGAGGAGGGATGGCCCTATGTGCCAATTTCACCTTGTCCACAGGCA	1629
Qy	2527	GGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCAT	2586
Db	1630	GGAAGTTGGGGAACCTTCAGGGAGATGAGGTTTGGAGTAAAGGGGCAATGTTTGCTCAT	1689
Qy	2587	GTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACA	2646
Db	1690	CTCAGGGGGTTGGGGGTTGAGGAAGGGCAGGCCCTGTCAGGAGCAAACATGAGT-ACCCA	1748
Qy	2647	GACAAGGCTATTGGAATCCACACCCCAAGAAACAAAGGGGTGAGCCCTGGACACCTCACCC	2706
Db	1749	CAGGAGGCCATCAGAACCCTCACCCCAAGAAACAAAGGGGTGAGCCCTGGGCACCCACAC	1808
Qy	2707	AG-----GATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGAC	2758
Db	1809	AGGGGTGACAGGATGTGGCTCCTTCTCATTTCTGATTCCAGATCTCAGTGAGGTGAGGAC	1868
Qy	2759	CTCATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAG	2818
Db	1869	CTTGTTCTCAGAGGTGACTCAGGTCAACACAGGGACCCCATCTGGTCTACAGACACAG	1928
Qy	2819	CGGTCCCAGGATCTGCCATGCGTTGCGGTGAGGAACATGAGGGAGGACTGAGGGTACCCC	2878
Db	1929	TGGTCCCAGGATCTGCCAAGAGTCCTGGTGAGGAATGTGAGGGAGGATTGAGGGTACCAC	1988
Qy	2879	AGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTCACCCAG	2938
Db	1989	AGGGCCAGAACGCAGATGATGACCCACAGAAATCAGCCCTGCTCCTGTTGTCACCCAG	2048
Qy	2939	AGAGCATGGGCTGGGCCGTCTGCCGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAG	2998
Db	2049	AGAGCATGGGCTTGGCTTTCTGCTGAGGTCCCTCTCTTATCCTGGGATCACTGGTGTCAC	2108
Qy	2999	GGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGG	3058
Db	2109	GGAGGGGGAGGCCTTGGTCTGAGGGGGCTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGG	2168
Qy	3059	CCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCA	3118
Db	2169	CTCTGCCAGGAGTTGAGGTGAGGACCAAGCAGGCTCCGCATCCAGGACACATGGGTTCCA	2228
Qy	3119	ATGAATTTTGATATCTCTTGCTGCCCTTC-CCCAAGGACCTAGGCACGTGTGGCCAGATG	3177
Db	2229	ATGAATTTTCGACATCTTTTGCTGTCGTTCTTCGGAAGACCTAGGCACAGGTGGCCAGATG	2288
Qy	3178	TTTGTCCCCTCCTGTCCTTCCATTCCATTATCATGGATGTGAACTCTTGATTGGATTCT	3237

Db	2289	TGGGGTTTCTTAGGTCTCT---GTTCCCTCTCAGGCATGTGAGCTCTTGATCTGAGTTTCT	2345
Qy	3238	CAGACCAGCAAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGA	3297
Db	2346	CAGGCCAGCAAAAAGAGTGGGATCCAGGCCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGA	2405
Qy	3298	GAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTACAGAGTCCAGCCCACCCTC	3357
Db	2406	ACACAGTGGGGATCATCCACTCCATGAGAGTGGGGACCTCACAGAGTCCAGCCTACCCTC	2465
Qy	3358	CTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATT	3417
Db	2466	TTGATGGCACTGAGGGACCGGGCTGTGCTTACAGTCTGCACCCTAAGGGCCCATGGATT	2525
Qy	3418	CCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAG	3477
Db	2526	CCTCTCCTAGGAGCTCCAGGAACAAGGCAGTGAGGCCTTGGTCTGAGACAGTGTCTCCTCAG	2585
Qy	3478	GTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACAC	3537
Db	2586	GTTACAGAGCAGAGGATGCACAGGCTGTGCCAGCAGTGAATGTTGCCCTGAATGCACAC	2645
Qy	3538	CAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTA	3597
Db	2646	CAAGGGCCCCACCTGCCACAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCTCCCTA	2705
Qy	3598	CTGTCAGTCCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACT	3656
Db	2706	CCATCAATCCTGCAGAATCGACCTCTGCTGGCCGGCTATAACCTGAGGTGCTCTCTCACT	2765
Qy	3657	TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC	3716
Db	2766	TCCTCCTTCAGGTTCTGAGCAGACAGGCCAA-CCGGAGGACAGGATTCCCTGGAGGCCAC	2824
Qy	3717	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT	3776
Db	2825	AGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCTAAGATTTGGT	2884
Qy	3777	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCC	3836
Db	2885	TCTCAGCTGAGGTCTCTCACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCC	2944
Qy	3837	AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	2945	AGCTTTTGCTGCTGCTGCTGCTGCCCTGAGCAGAGTCATCATGTCTCTTGAGCAGA	3004
Qy	3897	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Db	3005	AGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGG	3064
Qy	3957	TGTGTGTGCAGGCTGCCAC-----CTCCTCCTCCTCTCCTC	3992
Db	3065	TGGGTGCGCAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTC	3124
Qy	3993	TGGTCCTGGGCACCTTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTC	4052
Db	3125	TGGTCCCTGGCACCTTGGAGGAAGTGCTGCTGCTGAGTCAGCAGGTCTCCCCAGAGTC	3184
Qy	4053	CTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTG	4112
Db	3185	CTCAGGGAGCCTCTGCCTTACCACTACCATCAGCTTCACTTGTCTGGAGGCAACCCAATG	3244

; SEQ ID NO 147
; LENGTH: 4895
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-029-147

Query Match 44.3%; Score 2513.6; DB 9; Length 4895;
Best Local Similarity 79.9%; Pred. No. 0;
Matches 3415; Conservative 0; Mismatches 694; Indels 165; Gaps 32;

```
Qy      1478 ATGGTTCTGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAG 1537
      || || ||||| ||||| ||||| || || ||||| |||
Db      607 ATAGTCCTGAGGGGCCAGTTGAGATCGGCTGAGGGGAGCGGGCCCAAGCTCTGTGGCGAG 666

Qy      1538 GCAAGGTGAGATGCTGAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAA 1597
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      667 GCAAGGTGAGACTCTGAGGAAGGACTGAGGAGGCCCCACCCAAGATAGA-GGAACCCAA 725

Qy      1598 ATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAG 1657
      || ||||| | ||||| ||||| ||||| || |||||
Db      726 ATAATCCAGCCCACGTCTGCTGCCAGTCTTGGACCACCCGG---GGGAAGACTTCTCA- 781

Qy      1658 CTGGACCACCCCCGTCCTGCCCTGCCACTTAACCCACAGGGCAATCTGTAGTCATA 1717
      | | | | | | ||||| ||||| || | ||||| | |||||
Db      782 ---GGCTAGGCCATCCCAGCTCCCCTGCCACTAAAGCTACAGGGGACTCTAGAGTCA-- 836

Qy      1718 GCTTATGTGACCGGGCAGGGTTGGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGC 1777
                        |||| || | |||||
Db      837 -----AGAGCTTGGTGTGCCCAAGGCAGGGCCAGG 866

Qy      1778 ATCCGCCCCGGCATTAGGGTCAGGACCCTGGGAGGGAAGTGGGGTCCCCACCCACACCT 1837
      || || ||||| ||||| ||||| ||||| || ||||| |||||
Db      867 CTCTGCCTGGCATCGGGTCAGGACCTTGAGAGGGAAGTGGGGCGCTACACCCCAACC 926

Qy      1838 GTCTCCTCATCTCCACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCCAAC 1897
      | || | | | || || || ||||| || | || |||||
Db      927 CATCCGCATTC-----CAACATGCCAGCCCCATCCCCAATCCGTTTTCAGAA 976

Qy      1898 TCATCTTGTCAGAATCCCTGCTGTCAACCCACGGAAGCCACGGAATGGCGGCCAGGCAC 1957
      || || | ||||| ||||| ||||| || ||||| |||||
Db      977 TCCATTTTT---TCCCCTGAGTCAACCCGGAAGACCTGGGAATGGT---CAGGCAC 1029

Qy      1958 TCGGATCTTGACGTCCCATCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAACAG 2010
      ||||| ||||| ||||| || || || || ||||| |||||
Db      1030 TCGGATCTTGACATCCACATCGAGGGCTGAAGGAGGAGAGAGTTTGGTATCATGAGCAG 1089

Qy      2011 GGCCTCAGGGGAGCAGAGGGAG-----GGCCCTACTGCGAGATGAGGGAGGCCTCAGAG 2064
      ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1090 AGCCTCAGGGTAGCAGAGGGAGGACCCTGGCCCTCTGGGAGATGAGGAAGGCCTCAGGA 1149

Qy      2065 GACCCAGCACCC-----TAGGACACCGCACCCCTGTCTGAGACTGAG--GCTGCCA 2113
      ||||| ||||| || ||||| ||||| ||||| |||||
Db      1150 GACCCAGCACCCAAGGCAGGGAGCCACCCACCCCTGTCTGAGAATGAGGTGCCTCCT 1209

Qy      2114 CTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGA--CCCAG 2171
      | | | ||||| ||||| ||||| ||||| || ||||| |||||
Db      1210 CCTTTAGCCTCAGGAATCCAAGGGATGGCAACTCAGGTCAGCAGAGGGGTGGGTCCAAG 1269

Qy      2172 GCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGGAAATCCAGAT 2231
      ||| | ||| | | ||||| ||||| ||||| ||||| |||||
Db      1270 CCCTTCCAGGATCAAGGAAAGGAAGACGAGGGAGGATTGAGGGGCCTTGCATTCCAGAT 1329
```

Qy	2232	CAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTTC	2291
Db	1330	CAGTGGAGACCTGGGCCCTGGGAGGTCTGGGCAAGGTAGCCACCTGTAGCTCATACTTC	1389
Qy	2292	CTGCATCTTTGAGGT----GACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTC	2347
Db	1390	CTGCATCTTCGAGGTCACAGAGAGGAGAGGGCTATGGTCTGAGGGGTGGTACTTCAGGTC	1449
Qy	2348	AACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCC-CCCTTCATGAGGACT	2406
Db	1450	CGCAGAGGGAGGAGTCCCAGGATCTACAGGACCAAGGTGTGCCACACTTCACGAGGAAT	1509
Qy	2407	GGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTTTTAGTA	2466
Db	1510	GGGGATACCTGTGGCTCAGAAAGACGGGACCCACAGAGTCTGGCTGTCCCTGTTCTTA	1569
Qy	2467	GCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCA	2526
Db	1570	GCTCAGGGGGACCAGAGGAGGGATGGCCCTATGTGCCAATTCACTTGTTCACAGGCA	1629
Qy	2527	GGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCAT	2586
Db	1630	GGAAGTTGGGGAACCTTCAGGGAGATGAGGTTTTGGAGTAAAGGGGCAATGTTTGCTCAT	1689
Qy	2587	GTCAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACA	2646
Db	1690	CTCAGGGGGTTGGGGGTTGAGGAAGGGCAGGCCCTGTCAGGAGCAAACATGAGT-ACCCA	1748
Qy	2647	GACAAGGCTATTGGAATCCACACCCCAAGAAAGGGGTCAGCCCTGGACACCTCACCC	2706
Db	1749	CAGGAGGCCATCAGAACCCTCACCCCAAGAAAGGGGTCAGCCCTGGGCACCCACAC	1808
Qy	2707	AG-----GATGTGGCTTCTTTTTCCTCTGTTTCCAGATCTGGGGCAGGTGAGGAC	2758
Db	1809	AGGGGTGACAGGATGTGGCTCCTTCTCATTTCTGATTCCAGATCTCAGTGAGGTGAGGAC	1868
Qy	2759	CTCATTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAG	2818
Db	1869	CTTGTTCTCAGAGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTACAGACACAG	1928
Qy	2819	CGGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCC	2878
Db	1929	TGGTCCCAGGATCTGCCAAGAGTCTGTTGAGGAATGTGAGGGAGGATTGAGGGTACCAC	1988
Qy	2879	AGGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGTCTGTCACCCAG	2938
Db	1989	AGGGCCAGAACGCAGATGATGACCCACAGAAATCAGCCCTGTCTCTGTGTCACCCAG	2048
Qy	2939	AGAGCATGGGCTGGGCCGTCTGCCAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAG	2998
Db	2049	AGAGCATGGGCTTGGCTTCTGCTGAGGTCCCTCTCTTATCCTGGGATCACTGGTGTAC	2108
Qy	2999	GGACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGG	3058
Db	2109	GGAGGGGGAGGCCCTTGGTCTGAGGGGGCTGCACCCAGGTCAGTAGAGGGAGGGTCCCAGG	2168
Qy	3059	CCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCA	3118
Db	2169	CTCTGCCAGGAGTTGAGGTGAGGACCAAGCAGGCTCCGCATCCAGGACACATGGGTTCCA	2228

Qy 3119 ATGAATTTTGATATCTCTTGCTGCCCTTC-CCCAAGGACCTAGGCACGTGTGGCCAGATG 3177
 ||||| || ||| ||||| | || | | ||||| |||||
 Db 2229 ATGAATTTTCGACATCTTTTGCTGTCGTTCTTCGGAAGACCTAGGCACAGGTGGCCAGATG 2288

Qy 3178 TTTGTCCCCCTCCTGTCCTTCCATTCCATTATCATGGATGTGAACCTTTGATTGGATTCT 3237
 | | || |||| | || | ||| ||||| ||||| |||||
 Db 2289 TGGGGTTTCTTAGGTCCT---GTTCCCTCTCAGGCATGTGAGCTCTTGATCTGAGTTTCT 2345

Qy 3238 CAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGA 3297
 ||| ||||| || | ||||| ||||| || | ||||| |||||
 Db 2346 CAGGCCAGCAAAAGAGTGGGATCCAGGCCCTGCCCTGGAGAAATGTGAGGGCCCTGAGTGA 2405

Qy 3298 GAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTC 3357
 |||| |||| ||||| ||||| ||||| ||||| |||||
 Db 2406 ACACAGTGGGGATCATCCACTCCATGAGAGTGGGGACCTCACAGAGTCCAGCCTACCCTC 2465

Qy 3358 CTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCTGAGGGCCCGTGGATT 3417
 || | ||||| || ||||| ||||| | ||||| ||||| |||||
 Db 2466 TTGATGGCACTGAGGGACCGGGCTGTGCTTACAGTCTGCACCTAAGGGCCCATGGATT 2525

Qy 3418 CCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAG 3477
 |||| | ||||| ||||| ||||| ||||| ||||| |||||
 Db 2526 CCTCTCCTAGGAGCTCCAGGAACAAGGCAGTGAGGCCTTGGTCTGAGACAGTGTCTCAG 2585

Qy 3478 GTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACAC 3537
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2586 GTTACAGAGCAGAGGATGCACAGGCTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACAC 2645

Qy 3538 CAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTA 3597
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2646 CAAGGGCCCCACCTGCCACAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCTCCCTA 2705

Qy 3598 CTGTCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACT 3656
 | ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2706 CCATCAATCCTGCAGAATCGACCTCTGCTGGCCGGCTATACCCTGAGGTGCTCTCTCACT 2765

Qy 3657 TCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCAC 3716
 ||||| ||||| | || ||||| || ||||| ||||| ||||| |||||
 Db 2766 TCCTCCTTCAGGTTCTGAGCAGACAGGCCAA-CCGGAGGACAGGATTCCCTGGAGGCCAC 2824

Qy 3717 AGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCACT 3776
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2825 AGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTTAAGATTTGGT 2884

Qy 3777 TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCC 3836
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2885 TCTCAGCTGAGGTCTCTCACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCC 2944

Qy 3837 AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGATCATCATGTCTCTTGAGCAGA 3896
 |||| |||| |||| ||||| ||||| ||||| ||||| |||||
 Db 2945 AGCTTTTGCCCTGCACCTTGCTGCTGCTGAGCAGAGTCATCATGTCTCTTGAGCAGA 3004

Qy 3897 GGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG 3956
 |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3005 AGAGTCAGCACTGCAAGCCTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGG 3064

Qy 3957 TGTGTGTGCAGGCTGCCAC-----CTCCTCCTCCTCTCCTC 3992
 || ||| ||||| | || ||||| ||||| ||||| |||||
 Db 3065 TGGGTGCGCAGGCTCCTACTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCCTC 3124

Qy 3993 TGGTCCTGGGCACCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTC 4052

Db	3125	TTGGTCCCTGGCACCCCTGGAGGAAGTGCCTGCTGCTGAGTCAGCAGGTCCTCCCCAGAGTC	3184
Qy	4053	CTCAGGGAGCCTCCGCGCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTG	4112
Db	3185	CTCAGGGAGCCTCTGCCTTACCCACTACCATCAGCTTCACTTGCTGGAGGCAACCCAATG	3244
Qy	4113	AGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGT	4172
Db	3245	AGGGTTCCAGCAGCCAAGAAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAGTCCTTGT	3304
Qy	4173	TCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATC	4232
Db	3305	TCCGAGAAGCACTCAGTAACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTATC	3364
Qy	4233	GAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGC	4292
Db	3365	GAGCCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGAGTTCATCAAAAATTACAAGC	3424
Qy	4293	ACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTG	4352
Db	3425	GCTGCTTTCTTGATCTTCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTG	3484
Qy	4353	ACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCT	4412
Db	3485	ACGTGAAGGAAGTGGACCCACCAGCAACACCTACACCTTGTACCTGCCTGGGCCTTT	3544
Qy	4413	CCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTG	4472
Db	3545	CCTATGATGGCCTGCTGGGTAAATAATCAGATCTTTCCCAAGACAGGCTTCCTGATAATCG	3604
Qy	4473	TCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGC	4532
Db	3605	TCCTGGGCACAATTGCAATGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGC	3664
Qy	4533	TGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGC	4592
Db	3665	TGGGTGTGATGGGGGTGTATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAAAC	3724
Qy	4593	TGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTG	4651
Db	3725	TGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTACCCGGCAGTA	3784
Qy	4652	ATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGA	4711
Db	3785	ATCCTGCGCGCTATGAGTTCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGA	3844
Qy	4712	AAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGC	4771
Db	3845	AAGTCCTGGAGCATGTGGTCAGGGTCAATGCAAGAGTTCGCATTGCCATCCCATCCCTGC	3904
Qy	4772	GTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCA	4831
Db	3905	GTGAAGCAGCTTTGTTAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTG	3964
Qy	4832	GTGGGAGGG----GGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTT	4887
Db	3965	TGGGGAAGGGGCAGGGCTGGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCTT	4022
Qy	4888	GCCTCGTGTGACATGAGGCCCATTCCTCACTC----TGAAGAGAGCGGTTCAGTGTCTCA	4943

```

Db      4023 GCCTCGTGTAAACATGAGGCCCATCTCTCACTCTGTTTGAAGAAAATAGTCAGTGTCTTA 4082
Qy      4944 GTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGGAATT 5003
        ||||| ||||| || | |||| | ||||| ||||| ||||| ||||| |||||
Db      4083 GTAGTGGGTTTCTATTTTGTGGATGACTTGGAGATTTATCTCTGTTTCCCTTTTACAATT 4142
Qy      5004 GTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATG 5063
        ||| ||||| || | ||||| | ||||| | ||||| | ||||| | |||||
Db      4143 GTTGAAATG-TTCCTTTTAATGGATGGTTGAATTAACCTCAGCATCCAAGTTTATGAATC 4201
Qy      5064 ACAGCAGTCACACAGTTCTGTGTATATAGTTTAAAGGTAAGAGTCTTGTGTTTTATTTCAG 5123
        || | | | | | ||||| | ||||| | ||||| | ||||| | |||||
Db      4202 GTAGTTAACGTATATTGCTGTTAATATAGTTTAGGAGTAAGAGTCTTGTTTTTTATTTCAG 4261
Qy      5124 ATTGGGAAATCCATTCTATTTTGTGAATTGGG---ATAATAACAGCAGTGGAAATAAGTAC 5180
        ||||| ||||| ||||| ||||| || ||||| ||||| ||||| |||||
Db      4262 ATTGGGAAATCCGTTCTATTTTGTGAATTTGGGACATAATAACAGCAGTGGAGTAAGTAT 4321
Qy      5181 TTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAATTAAGAG 5240
        ||||| |||| | || | ||||| ||||| | ||||| ||
Db      4322 TTAGAAGTGTG---AATTCACCGTGAAATAGGTGAGAT-----AAATTAAG 4366
Qy      5241 ATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATATGCAT 5300
        ||| | |||| | ||||| | ||||| | ||||| | ||||| | |||||
Db      4367 ATACTTAATTCCCGCCTTATGCCTCAGTCTATTCTGTAAAATTTAAAAATATATATGCAT 4426
Qy      5301 ACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTC 5360
        ||||| ||||| ||||| | ||||| | ||||| | ||||| | |||||
Db      4427 ACCTGGATTTCCCTTGCTTC---GTGAATGTAAGAGAAATTAAATCTGAATAAATAATTC 4483
Qy      5361 TTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGGGAAGGCCCT 5420
        || ||||| ||||| | ||||| | ||||| | ||||| | |||||
Db      4484 TTTCTGTTAACTGGCTCATTTCTTCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCA 4543
Qy      5421 GGGTTAGTAGTGGAGATGCTAAGGTAAAGCCAGACTCATACCCACCCATAGGGTCGTAGAG 5480
        || ||||| ||||| ||| ||||| ||||| || ||| ||| ||||| ||
Db      4544 GGATTAGTAGTGGAGATACTAGGGTAAGCCAGACACACACCTACCGATAGGGTATTAAGA 4603
Qy      5481 TCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAGGGAAAA 5540
        | | | |||| |||| | |||| | ||||| ||||| |||||
Db      4604 GTCTAGGAGCGCGGTCATATAATTAAGGTGACAAGATGTCTCTAAGATGTAGGGAAAA 4663
Qy      5541 GTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGA 5600
        || | | | |||| | ||||| | ||||| | |||| | ||||
Db      4664 GT----AACGAGTGTGGGTATGGGGCTCCAGGTGAGAGTGGTCGGGTGTAAATTCCCTGT 4719
Qy      5601 GCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTGTAATGA 5660
        | ||||| ||||| ||||| || || ||||| |||| | |||||
Db      4720 G-TGGGGCCTTTTGGGCTTTGGGAAACTCCATTTTCTTCTGAGGGATCTGATTCTAATGA 4778
Qy      5661 TCTTGGGTGGATCC 5674
        | |||| |||
Db      4779 AGCTTGGTGGGTCC 4792

```

```

RESULT 4
US-10-482-029-87
; Sequence 87, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S

```

```

; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 4741
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-029-87

```

```

Query Match          42.7%; Score 2422.8; DB 9; Length 4741;
Best Local Similarity 75.7%; Pred. No. 0;
Matches 3726; Conservative 0; Mismatches 882; Indels 314; Gaps 46;

```

```

Qy      715 TTCCCGCCAGGAAACATCCGGGTGCCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGG 774
      ||| ||||| || | ||||| || ||||| ||||| ||||| ||| ||
Db      15 TTCAACCCAGGGAATCCCTGGGTGACCAGATGTGGTGCCACTGTCTTGCACATTTGAGGT 74

Qy      775 CAGAGAGAAGCGAGGTTTCCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGA 834
      | ||||| ||| | || |||| | || || || || || || || ||
Db      75 CGGAGAGAAGCAAGGGCTCGCTCTCAGGGGCAGC-TGGAGATCAGCTGAGGGCAGCTGG 133

Qy      835 CCCAGGCTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTC 894
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||| ||
Db      134 CCCTGGCTCTGTGAGGATGCAAGGTGAGATGCTGAGGGAGGACTAAGGAGTATCCCACCC 193

Qy      895 CAAATAGAGAGCCCCAAATATTCCAG---CCCCGCCCTTGCTGCCAGCCCTGGCCCCACCC 951
      | ||| | ||||| ||||| | || | ||||| ||| |||| ||| ||
Db      194 CTGGTAGTGAGACCCCAAATAATCCAGTGCCACCTCTCCTGCTGCTAGCTCTGGACCATCC 253

Qy      952 GCGGGAAGACGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGAC 1011
      || | || || || || ||||| ||||| |||| | |||| | |||
Db      254 AGGGCAGGACTTCTTAGGCTGGGCCACCCCCAGTCCCCCACCCTTAAGCCGCAGGGGA- 312

Qy      1012 ACCAGGTTCTTCTCCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGT 1071
      ||| ||| ||||| ||| | ||||| ||||| ||||| ||||| |||||
Db      313 -----CTCAGGAGACAGAGCTTGGTATGACCAGGGCAGGACTGGT 352

Qy      1072 TAGGAGAGGGCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGC 1131
      ||||| ||| | || ||||| ||||| | ||| |||| | || | ||| |
Db      353 TAGGAGAGGACAGTCCCA-GCTCTGCCAGGAAACAACGTCAGGAACCTAAGGGAAAGCT 411

Qy      1132 TGTGGGCCCCCAAGACTGCACTCCAATCCCCACTCCCACCCCATTCGCATTCCCATTCCC 1191
      | ||||
Db      412 GAGGCTACCCC----- 422

Qy      1192 CACCCAACCCCCATCTCCTCAGCTACACCTCCACCCCCATCCCTACTCCTACTCCGTCAC 1251
      |||| | | | | || ||| |||| | |||
Db      423 -----CACCCAACTCTATTCTGTCCCTACCTCCGTCC 457

Qy      1252 CTGACCACCACCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCTCACT 1311
      | ||| |||| ||| || || |||| |||| | ||||| ||| |||
Db      458 CCCACCTACACCCCCATTCC-----CCCACCCCTTCCCTACCGGCACCTCTATCCCACA 512

Qy      1312 GCCCCCAACCCACCCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTTCTG 1371
      ||||| ||||| ||| |||
Db      513 TCCCCCA-----CCCCATCCTG 530

Qy      1372 GCAGAATCCGGTT-TGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAA 1430

```

Db	531	GCAGAATCCGATTCTGCCCCTGATTTCAACCCAGGGAAGCCCTAGGGGGCCGGATGTGAT	590
Qy	1431	ACCACTGACTTGAACCTCACAGATCTGAGAGAAGCCAGGTTTCATTTAATGGTTCTGAGGG	1490
Db	591	GCTGCTGACTTGTGCATTGGGGGTCAGAGAGAATCAAGG-----GCATGGTTCTGAGAA	644
Qy	1491	GCGGCTTGAGATCCACTGAGGGGAGTGGTTTATAGGCTCTGTGAGGAGGCAAGGTGAGATG	1550
Db	645	GCCGACTTGAGATCAGCAGAGGGGAATGGGCCCGGGCTCTGTGAGGAGGCAAGGTGAGACC	704
Qy	1551	CT-GAGGGAGGACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTAC	1609
Db	705	CCCGAGGAAGGAATGAGGAAGCCCTCACCC--AGATAGAGAACCCCAAATAATCCAGTAC	762
Qy	1610	CACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCC	1669
Db	763	TACCTTTGCTGCCAGCCCTGGACCAC----CCAGGGCAGACTTCTCAGGCTGAACCTTCC	818
Qy	1670	CCGTCCCGTCCCACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTT-ATGTGAC	1728
Db	819	C---CCCTCCCCACTGCCACTTAAGCCACAAGGGACTCTGGAGTCAGACCTTGGTGTGAC	875
Qy	1729	CGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCCAGGCATCAAGGTCCAGCATCCGCCCGGC	1788
Db	876	CAGGGAAGGGCCGGTCAGGAGAGG-----GCAGGGGCCAGGCTCTGTCTAGGC	922
Qy	1789	ATTAGGGTCAGGACCCTGGGAGGGAAGTGAAGGTTCCCCACCCACACCTGTCTCCTCATC	1848
Db	923	ATCAAAATCAGGACCCTGAGAGAGAATTGAGGGCCCCACCCCAACCCCTATACCCATCC	982
Qy	1849	TCCACCGCCACCCCACTCACATTCCCATACCTACC----CCCTACCCCCAACCTCATCTT	1904
Db	983	CTAACCCCATACCCACTCTACTTGCATTCCAGCCCCATCCCCACACCTACCCCATCTT	1042
Qy	1905	GTCAGAA-----TCCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGG	1954
Db	1043	GGCAGAATCTGTTTCTTTCCCTGCAGTCAACCCACAGAAGCCCCAGGAATGACAGACAGG	1102
Qy	1955	CACCTCGGATCTTGACGTCCCCTCCAGGGTCTGATGGAGGGAAGGG-----GCTTGAA	2007
Db	1103	CACACCTATCTTGACGTCCACATCCAGGGCTGAAGGAGGGAAGGGCTTAGTATCATGAG	1162
Qy	2008	CAGGGCTCAGGGGAGCAGAGG----GAGGGCCCTACTGCGAGATGAGGGAGGCCTCAGA	2063
Db	1163	CAGGGCTCAGGGGAGTCTCTGCTCCTCAAGCCCTGCTGGGAGTAAAGGGAGGCCTCAGG	1222
Qy	2064	GGACCCAGCACCCCTAGGA-----CACCGCACCCCTGTCTGAGACTGAG--GCTGCC	2112
Db	1223	GAACCCAGGTCCCTCAGGATAGGGGTTCCACTCCAACCTGTCTGAGACTGAGGCGCCTCC	1282
Qy	2113	ACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGACCCAGG	2172
Db	1283	TCTTTTCATCCTCGGGAATCACAGGGATGGAGACTCACGTACGAGAGGGTGGGGCCCAAC	1342
Qy	2173	CCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGAATCCAGATC	2232
Db	1343	CCTGCCAGGATCAAGGAGAGGAAGAAGAGGGAGGACTCAGGGTACCTTTGAGTCCAGAAC	1402
Qy	2233	AGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTCC	2292

Db 1403 AATGGGGACCTTTGCCCTGGGAGGTCCAGTGCACAGTGGCCACCTGTAGCCCATGCTTGC 1462

Qy 2293 TGCATCTTTGAGGTGAC----AGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCA 2348
 |||| ||| ||||| |||| || ||||| ||| |||| | |||||

Db 1463 TGCACCTTCTGGGTGACAAAGAGGAGAGGGCTGTGGTCAGAGCAGTGGTGACTCAGGTCA 1522

Qy 2349 ACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATGAGGACTGG 2408
 ||||| |||| ||| | |||| ||||| ||||| || |||

Db 1523 GCAGAGGGAGGAGTCCCAGCATCTGCAGGCCCAATGTGTGCCCCATTCATGAAGATTGG 1582

Qy 2409 GGATATCCCCGGCTCAGAAAAGAGGGACTCCACACAGTCTGGCTGTCCCCTTTTAGTAGC 2468
 |||| || ||||| ||||| ||||| ||||| ||||| ||||| || |||

Db 1583 GGATA-CCTTGGCTCAGAAAAGAGGGACCCACAGAGTCTGGCTGTCCCCTGATTTTTGC 1641

Qy 2469 TCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCATTGTACCACAGGCAGG 2528
 || ||||| |||| |||| || |||| ||| |||| ||||| |||

Db 1642 TCAGAGGGGACCAAATCAAGGATAGCCCTATGTGCCAACCTCATTTGTGCCACAGGAAAG 1701

Qy 2529 AAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGT 2588
 ||||| | ||||| ||||| ||||| ||||| || ||| ||||| |

Db 1702 AAGTTGAAGAGCCCTCAGGGTGATGGGGTCTTGACAGTAAAGGGGAGCTATCTGCTCATCT 1761

Qy 2589 CAGGGAATTGGGGGTTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGA 2648
 |||| || ||||| ||||| |||| | || || || ||| |||

Db 1762 CAGGGGGTTTCAGGTTGAGGAATGGCAGGCCCATCACGATGAAGAGTAACCCACAGG-- 1819

Qy 2649 CAAGGCTATTGGAATCCACACCCCAAGAAAGGGGTACGCCCTGGACACCTCA----- 2703
 || || | || | ||||| ||||| ||||| ||||| |||

Db 1820 ---AGCCATAGAAACACTACCCCAAGAAAGGGGTACATACCTGGACACCCCATGTGG 1876

Qy 2704 ----CCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACC 2759
 ||||| || || | || ||||| ||||| ||| ||||| |||

Db 1877 GGGTGACAGGATGTAGC-TCCATCTCATTCTGTTTTTCAGATCTCGGGGAGGTGAGGAAC 1935

Qy 2760 TCATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCATCTGGTCTAAAGACAGAGC 2819
 | |||| |||| ||||| ||||| |||| ||||| ||| |||||

Db 1936 TTGTTCTCCGAGGATGACTCAGGTCAACACAGGGGCCCATCTGGTGGATAGACAGAGT 1995

Qy 2820 GGTCCCAGGATCTGCCATGCGTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCA 2879
 ||||| || || ||||| ||||| ||||| ||||| || |||||

Db 1996 GGTCCCAGGATCTGTCTAGTAGTTCCGGTGAGGAACATGAGGGACGATTGAGGGCACCTT 2055

Qy 2880 GGACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCTGCTGTACCCCA 2939
 || ||||| || || || || ||||| ||||| ||||| |||||

Db 2056 GGGCCAGAACACAGATGAGGACCTCACGGAATCTGCCCTGCCCTGCTGTCACTCCAGA 2115

Qy 2940 GAGCATGGGCTGGGCCGTCTGCCGAGGTCTTCC--GTTATCCTGGGATCATTGATGTCA 2997
 ||||| |||| |||| | |||| || ||||| ||||| |||||

Db 2116 GAGCATGGGCAGGGCTGTCTGTCTGCAGTCCCCCACTTACCCTGGGATCATTTGGTGTCA 2175

Qy 2998 GGGACGGGGAGGCCTTGGTCTGAGAAGGCTGCGCTCAGGTGAGTAGAGGGAGCGTCCAG 3057
 |||| ||||| || |||| || |||| ||||| ||||| |||||

Db 2176 GGGATGGGGAGGTCTTTGTC-GAGGGGTCTGCACTCAGGTGAGTAGAGGGAGCGTCTTAG 2234

Qy 3058 GCCCTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCC 3117
 ||||| ||||| |||| || |||| || ||||| ||||| |||||

Db 2235 GCCCTGCCAGGAGACAAGGTAAAGAACGAAGCAGGTTCTCACCCAGGACACATGAATTCC 2294

Qy 3118 AATGAATTTTGATATCTCTTGCTGCCCTTCCCA-AGGACCTAGGCACGTGTGGCCAGAT 3176
 |||| |||| ||||| || ||||| || ||||| ||||| |||||

Db 2295 AATGCATTTTCAGCATCTCTTCTGTCTTCCCAAGAGGACCTGGGCACGTGTGGCCAGAT 2354

Qy	3177	GTTCGTCCCTCCTGTCCTTCCATTCTTATCATGGATGTGAACCTTTGATTTGGATTTC	3236
Db	2355	GTGAGTCTCCTCATGTCCT--GTTCCCTATCAGGGATGTGAGCTCTTAATCTGAGTTTC	2411
Qy	3237	TCAGACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTG	3296
Db	2412	TCAGGCCAGCAAAAGGGTGGGATCCAGGCCCTGCCAGGAGAAAGGTGAGGGCCCTGTGTG	2471
Qy	3297	AGAACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCT	3356
Db	2472	AGCACAGAGGGGACCATTACCCCAAGAGGTGGAGACCTCACAGATTCCAGCCTACCCT	2531
Qy	3357	CCTGGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGAT	3416
Db	2532	CCTGTTAGCACTGGGGGCCCTGAGGCTGTGCTTGCACTCTGCACCCTGAGGGCCCATGCAT	2591
Qy	3417	TCCTCTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCA	3476
Db	2592	TCCTCTTCCAGGAGCTCCAGGAACAGACACTGAGGCCTTGGTCTGAGGCCGTGCCCTCA	2651
Qy	3477	GGTCACAGAGCAGAGGATGCACAGGGT----GTGCCAGCAGTGAATGTTTGCCCTGAATG	3532
Db	2652	GGTCACAGAGCAGAGGAGATGCAGACGTCTAGTGCCAGCAGTGAACGTTTGCCCTGAATG	2711
Qy	3533	CACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCA-CC	3591
Db	2712	CACACTAATGGCCCCCATCGCCCCAGAACATATGGGACTCCAGAGCACCTGGCCTCACCC	2771
Qy	3592	TCCCTACTGTCTAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTC	3651
Db	2772	TCTCTACTGTCTAGTCCTGCAGAATCAGCCTCTGCTTGCTTGTGTACCCTGAGGTGCCCTC	2831
Qy	3652	TCACTTCCTCCTTCAGGTTTTTCAGGGGACAGGCCAACCCAGAGGAC-----A	3698
Db	2832	TCACTTTTTCTCCTTCAGGTTCTCAGGGGACAGGCTGACCAGGATCACCAGGAAGCTCCAGA	2891
Qy	3699	GGATTCCCTGGAGGCCACAGAGGAGCACC-AAGGAGAAGATCTGTAAGTAGGCCTTTGTT	3757
Db	2892	GGATCCCCAGGAGGCCCTAGAGGAGCACCAAGGAGAAGATCTGTAAGTAAGCCTTTGTT	2951
Qy	3758	AGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGC	3817
Db	2952	AGAGCCTCCAAGGTTTCAGTTTTTAGCTGAGGCTTCTCACATGCTCCCTCTCTCTCCAGGC	3011
Qy	3818	CTGTGGGTCTTCATTGCCAGCTCCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTC	3877
Db	3012	CAGTGGGTCTCCATTGCCAGCTCCTGCCACACTCCTGCCTGTTGCGGTGACCAGAGTC	3071
Qy	3878	ATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAA	3937
Db	3072	GTCATGTCTCTTGAGCAGAAGAGTCAGCACTGCAAGCCTGAGGAAGGCCCTTGACACCCAA	3131
Qy	3938	CAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC-----C	3976
Db	3132	GAAGAGGCCCTGGGCCTGGTGGGTGTGCAGGCTGCCACTACTGAGGAGCAGGAGGCTGTG	3191
Qy	3977	TCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACA	4036
Db	3192	TCCTCCTCCTCTCCTCTGGTCCCAGGCACCCTGGGGGAGGTGCCTGCTGCTGGGTCAACA	3251

Qy	4037	GATCCTCCCCAGAGTCTCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGA	4096
Db	3252	GGTCCTCTCAAGAGTCTCTCAGGGAGCCTCCGCCATCCCCACTGCCATCGATTTCACCTCTA	3311
Qy	4097	CAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGT	4156
Db	3312	TGGAGGCAATCCATTAAGGGCTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTCCCCT	3371
Qy	4157	ATCCTGGAGTCCTTGTTCAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTT	4216
Db	3372	GACCCAGAGTCTGTGTTCCGAGCAGCACTCAGTAAGAAGGTGGCTGACTTGATTCATTTT	3431
Qy	4217	CTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTC	4276
Db	3432	CTGCTCCTCAAGTATTAAGTCAAGGAGCTGGTCACAAAGGCAGAAATGCTGGAGAGCGTC	3491
Qy	4277	ATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCAG	4336
Db	3492	ATCAAAAATTACAAGCGCTGCTTTCTGAGATCTTCGGCAAAGCCTCCGAGTCCTTGCAG	3551
Qy	4337	CTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCCCACGGCCACTCCTATGTCCTTGTC	4396
Db	3552	CTGGTCTTTGGCATTGACGTGAAGGAAGCGGACCCCCACAGCAACACCTACACCCTTGTC	3611
Qy	4397	ACCTGCCTAGGTCTCTCCTATGATGGCTTGCTGGGTG---ATAATCAGATCATGCCCAAG	4453
Db	3612	ACCTGCCTGGG---ACTCCTATGATGGCTTGCTGGTTGATAATAATCAGATCATGCCCAAG	3669
Qy	4454	ACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAG	4513
Db	3670	ACGGGCCCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGGCAAATGCGTCCCTGAG	3729
Qy	4514	GAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCC	4573
Db	3730	GAGGAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTC	3789
Qy	4574	TATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTA-	4632
Db	3790	TGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTAC	3849
Qy	4633	CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTC	4692
Db	3850	CGGCAGGTGCCAGCAGTGATCCCATATGCTATGAGTTACTGTGGGGTCCAAGGGCACTC	3909
Qy	4693	GCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGC	4752
Db	3910	GCTGCT-----TGAAAGTACTGGAGCACGTGGTCAGGGTCAATGCAAGAGTTCTC	3959
Qy	4753	TTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCA	4812
Db	3960	ATTTCTTACCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCA	4019
Qy	4813	TGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGT	4872
Db	4020	TGAGCTGCAGCCAGGGCCACTGCGAGGGGGGCTGGGCCAGTGCACCTTCCAGGGCTCCGT	4079
Qy	4873	CCAGCAGCTTCCCCTGCC-TCGTGTGACATGAGGCCATTCTTCACTC--TGAAGAGAGC	4929
Db	4080	CCAGTAGTTTCCCCTGCCTTAATGTGACATGAGGCCATTCTTCTCTTTGAAGAGAGC	4139
Qy	4930	GGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGT	4989

Db	4140	AGTCAACATTCTTAGTAGTGGGTTTCTGTTCTATTGGATGACTTTGAGATTTGTCTTTGT	4199
Qy	4990	TCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATC	5049
Db	4200	TTCTTTTGGGAATTGTTCAAATG-TTTCTTTTAATGGGTGGTTGAATGAAC TTCAGCATT	4258
Qy	5050	CAAGTTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGT	5107
Db	4259	CAAATTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGT	4318
Qy	5108	CTTGTGTTTTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAG	5165
Db	4319	CTTGTTTTTTATTCAGATTGGGAAATCCATTCCATTTTGTGAATTGGGACATAGTTACAG	4378
Qy	5166	CAGTGGAATAAGTACTTA-GAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAA	5224
Db	4379	CAGTGGAATAAGTATTCATTTAGAAATGTGAATGAGCAGTAAAAC TGATGACA-----	4431
Qy	5225	CTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAATTT	5284
Db	4432	-TAAAGAAATTAAGAGATATTTAATTCTTGCTTATACTCAGTCTATTCGGTAAATTTTT	4490
Qy	5285	TTAAAGATATATGCATACCTGGATTTCTTGCTTCTTTGAGAATGTAAGAGAAATTAAA	5344
Db	4491	TTTAAAAAATGTGCATACCTGGATTTCTTGCTTCTTTGAGAATGTAAGACAAATTAAA	4550
Qy	5345	TCTGAATAAAGAATTCTTCCTGTTCAGTGGCTCTTTTCTTCTCCATGCACTGAGCATCTG	5404
Db	4551	TCTGAATAAATCATCTCCCTGTTCAGTGGCTCATTTATTCTCTATGCACTGAGCATTTG	4610
Qy	5405	CTTTTTGGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCAC	5464
Db	4611	CTCTGTGGAAGGCCCTGGGTTAATAGTGGAGATGCTAAGGTAAGCCAGACTCACCCCTAC	4670
Qy	5465	CCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCT	5524
Db	4671	CCACAGGGTAGTAAAGTCTAGGAGCAGCAGTCATATAATTAAGGTGGAGAGATGCCCTCT	4730
Qy	5525	AA 5526	
Db	4731	AA 4732	

RESULT 5

US-10-117-937-81

; Sequence 81, Application US/10117937

; Publication No. US20030220239A1

GENERAL INFORMATION:

; APPLICANT: CTL IMMUNO THERAPIES CORP.

; APPLICANT: SIMARD, John, J.L.

; APPLICANT: DIAMOND, David, C.

; APPLICANT: LIU, Liping

; APPLICANT: XIE, Zhidong

; TITLE OF INVENTION: EPITOPE SEQUENCES

; FILE REFERENCE: CTLIMM.027A

; CURRENT APPLICATION NUMBER: US/10/117,937

; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: US 60/282,211

; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: US 60/337,017

; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-117-937-81

Query Match 42.4%; Score 2408; DB 7; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db       1  GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61  ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          |||
Db     121  CAGGGCTGTGCTTGCGGTCTGCACCCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db     181  GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db     241  CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          |||
Db     301  CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
          |||
Db     361  CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
          |||
Db     421  GGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          |||
Db     481  GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 3855
          |||
Db     541  CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 600

Qy      3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
          |||
Db     601  GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy      3916 TGAGGAAGCCCTTGAGGCCCCAACAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
          |||
```

Db 661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy 3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035
 |||

Db 721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780

Qy 4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG 4095
 |||

Db 781 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG 840

Qy 4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 4155
 |||

Db 841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 900

Qy 4156 TATCCTGGAGTCCTTGTTCGAGCAGTAATCATAAGAAGGTGGCTGATTGGTTGGTTT 4215
 |||

Db 901 TATCCTGGAGTCCTTGTTCGAGCAGTAATCATAAGAAGGTGGCTGATTGGTTGGTTT 960

Qy 4216 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 4275
 |||

Db 961 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 1020

Qy 4276 CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 4335
 |||

Db 1021 CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 1080

Qy 4336 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 4395
 |||

Db 1081 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 1140

Qy 4396 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 4455
 |||

Db 1141 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 1200

Qy 4456 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 4515
 |||

Db 1201 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 1260

Qy 4516 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 4575
 |||

Db 1261 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 1320

Qy 4576 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG 4634
 |||

Db 1321 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG 1380

Qy 4635 GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC 4694
 |||

Db 1381 GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC 1440

Qy 4695 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT 4754
 |||

Db 1441 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT 1500

Qy 4755 TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG 4814
 |||

Db 1501 TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG 1560

Qy 4815 AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC 4874
 |||

Db 1561 AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC 1620

Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	1740
Qy	4995	TTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	5054
Db	1741	TTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATT CAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATT CAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAC TGAGCATCTGCTTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAC TGAGCATCTGCTTTTTGGAA	2160
Qy	5415	GGCCCTGGGT TAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGT TAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG	5534
Db	2221	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG	2280
Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG	2340
Qy	5595	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400
Qy	5655	TAATGATCTTGGGTGGATCC	5674
Db	2401	TAATGATCTTGGGTGGATCC	2420

RESULT 6

US-10-741-466-5

; Sequence 5, Application US/10741466

```

; Publication No. US20040180058A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; APPLICANT: Shneider, A.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003
; CURRENT APPLICATION NUMBER: US/10/741,466
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-741-466-5

```

```

Query Match          42.4%;  Score 2408;  DB 9;  Length 2420;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 2419;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;

```

```

Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 3435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 3855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 600

```

Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500

Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	1740
Qy	4995	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	2160
Qy	5415	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280
Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATG	2340
Qy	5595	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400
Qy	5655	TAATGATCTTGGGTGGATCC	5674

Db 2401 TAATGATCTTGGGTGGATCC 2420

RESULT 7

US-10-657-022-81
; Sequence 81, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANNK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-657-022-81

Query Match 42.4%; Score 2408; DB 9; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	3256	GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC	3315
Db	1	GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC	60
Qy	3316	ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC	3375
Db	61	ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC	120
Qy	3376	CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA	3435
Db	121	CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA	180
Qy	3436	GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	3495
Db	181	GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	240
Qy	3496	CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	3555
Db	241	CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	300
Qy	3556	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT	3615
Db	301	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT	360
Qy	3616	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTCAG	3675
Db	361	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTCAG	420
Qy	3676	GGGACAGGCCAACCCAGAGGACAGGATTCCTGGAGGCCACAGAGGAGCACCAGGAGAA	3735

Db	421	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	480
Qy	3736	GATCTGTAAGTAGGCCTTTGTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	3795
Db	481	GATCTGTAAGTAGGCCTTTGTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	540
Qy	3796	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT	3855
Db	541	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT	600
Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380

Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	1740
Qy	4995	TTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741	TTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGAAT	5174
Db	1861	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	2160
Qy	5415	GGCCCTGGGTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280

```

Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 5594
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 2340

Qy      5595 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
          ||||||||||||||||
Db      2401 TAATGATCTTGGGTGGATCC 2420

```

RESULT 8

```

US-10-807-308-17
; Sequence 17, Application US/10807308
; Publication No. US20040241725A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Wenming
; APPLICANT: Dong, Gang
; TITLE OF INVENTION: LUNG CANCER DETECTION
; FILE REFERENCE: 114122-00153
; CURRENT APPLICATION NUMBER: US/10/807,308
; CURRENT FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-807-308-17

```

```

Query Match          42.4%; Score 2408; DB 9; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

```

Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCAATCC 3315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1    GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCAATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61   ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGATTCTCTTCCTGGAGCTCCA 3435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121  CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGATTCTCTTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181  GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  CACAGGGTGTGCCAGCAGTGAATGTTTGGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301  CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTCAG 3675

```

Db	361		CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTCAG	420
Qy	3676		GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	3735
Db	421		GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	480
Qy	3736		GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	3795
Db	481		GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	540
Qy	3796		CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	3855
Db	541		CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	600
Qy	3856		GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601		GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916		TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661		TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976		CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721		CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036		AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781		AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096		ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841		ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156		TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901		TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216		TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961		TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276		CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021		CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336		GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081		GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396		CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141		CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456		AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGA	4515
Db	1201		AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGA	1260
Qy	4516		GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575

Db 1261 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 1320

Qy 4576 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG 4634
 |||

Db 1321 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG 1380

Qy 4635 GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC 4694
 |||

Db 1381 GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC 1440

Qy 4695 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT 4754
 |||

Db 1441 TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT 1500

Qy 4755 TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG 4814
 |||

Db 1501 TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG 1560

Qy 4815 AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC 4874
 |||

Db 1561 AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC 1620

Qy 4875 AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA 4934
 |||

Db 1621 AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA 1680

Qy 4935 GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT 4994
 |||

Db 1681 GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT 1740

Qy 4995 TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT 5054
 |||

Db 1741 TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT 1800

Qy 5055 TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT 5114
 |||

Db 1801 TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT 1860

Qy 5115 TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT 5174
 |||

Db 1861 TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT 1920

Qy 5175 AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT 5234
 |||

Db 1921 AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT 1980

Qy 5235 TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 5294
 |||

Db 1981 TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 2040

Qy 5295 ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 5354
 |||

Db 2041 ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 2100

Qy 5355 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA 5414
 |||

Db 2101 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA 2160

Qy 5415 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 5474
 |||

Db 2161 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 2220

```

Qy      5475 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 5534
          |||
Db      2221 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 2280

Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 5594
          |||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 2340

Qy      5595 CCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
          |||
Db      2341 CCCTGAGCTGGGGCATTGTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
          |||
Db      2401 TAATGATCTTGGGTGGATCC 2420

```

RESULT 9

```

US-10-866-484-5
; Sequence 5, Application US/10866484
; Publication No. US20050013826A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, M.
; APPLICANT: Shneider, A.
; TITLE OF INVENTION: Vaccine Compositions and Methods
; FILE REFERENCE: 25955-003CIP
; CURRENT APPLICATION NUMBER: US/10/866,484
; CURRENT FILING DATE: 2004-06-11
; PRIOR APPLICATION NUMBER: 60/435,500
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 10/741,466
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Influenza A virus
US-10-866-484-5

```

```

Query Match          42.4%; Score 2408; DB 9; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

```

Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db      1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTTCTTCTGGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTTCTTCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

```

Qy	3496	CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	3555
Db	241	CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	300
Qy	3556	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT	3615
Db	301	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT	360
Qy	3616	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	3675
Db	361	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	420
Qy	3676	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	3735
Db	421	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	480
Qy	3736	GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCCTCAGCTGAGGCCTCTCA	3795
Db	481	GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCCTCAGCTGAGGCCTCTCA	540
Qy	3796	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT	3855
Db	541	CACACTCCCTCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT	600
Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCTTGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455

Db	1141	CACCTGCCTAGGTCTCTCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAAATGTCTGCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAAATGTCTGCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	1740
Qy	4995	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	5054
Db	1741	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAT	5174
Db	1861	TTTATTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCC TTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCC TTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354

```

Db      2041 ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 2100

Qy      5355 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA 5414
|||||
Db      2101 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA 2160

Qy      5415 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 5474
|||||
Db      2161 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 2220

Qy      5475 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 5534
|||||
Db      2221 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 2280

Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 5594
|||||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 2340

Qy      5595 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
|||||
Db      2341 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
|||||
Db      2401 TAATGATCTTGGGTGGATCC 2420

```

RESULT 10

```

US-10-482-029-91
; Sequence 91, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-029-91

```

```

Query Match          42.4%;  Score 2408;  DB 9;  Length 2420;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 2419;  Conservative 0;  Mismatches 0;  Indels 1;  Gaps 1;

```

```

Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
|||||
Db      1    GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
|||||
Db      61   ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTTCTTCTGGAGCTCCA 3435
|||||
Db      121  CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTTCTTCTGGAGCTCCA 180

```

Qy	3436	GGAACCAGGCAGTGAGGCC TTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	3495
Db	181	GGAACCAGGCAGTGAGGCC TTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	240
Qy	3496	CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	3555
Db	241	CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	300
Qy	3556	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCCTGTAGAAT	3615
Db	301	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCCTGTAGAAT	360
Qy	3616	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	3675
Db	361	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	420
Qy	3676	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	3735
Db	421	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	480
Qy	3736	GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	3795
Db	481	GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	540
Qy	3796	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	3855
Db	541	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	600
Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGT	4395

Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	1740
Qy	4995	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294

```

Db      1981 TAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT 2040
Qy      5295 ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 5354
        |||
Db      2041 ATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA 2100
Qy      5355 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA 5414
        |||
Db      2101 GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA 2160
Qy      5415 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 5474
        |||
Db      2161 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 2220
Qy      5475 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG 5534
        |||
Db      2221 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG 2280
Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 5594
        |||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 2340
Qy      5595 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
        |||
Db      2341 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400
Qy      5655 TAATGATCTTGGGTGGATCC 5674
        |||
Db      2401 TAATGATCTTGGGTGGATCC 2420

```

RESULT 11

US-10-871-708-14

; Sequence 14, Application US/10871708

; Publication No. US20050118186A1

; GENERAL INFORMATION:

; APPLICANT: Chiang, Chih-Sheng

; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

; TITLE OF INVENTION: ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS

; FILE REFERENCE: MANNK.035A

; CURRENT APPLICATION NUMBER: US/10/871,708

; CURRENT FILING DATE: 2004-06-17

; PRIOR APPLICATION NUMBER: 60/479,554

; PRIOR FILING DATE: 2003-06-17

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 14

; LENGTH: 2420

; TYPE: DNA

; ORGANISM: Human antigen (MAGE-1) gene, complete cds

US-10-871-708-14

```

Query Match          42.4%; Score 2408; DB 10; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

```

Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
        |||
Db      1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60
Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375

```

Db	61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC	120
Qy	3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA	3435
Db	121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA	180
Qy	3436 GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	3495
Db	181 GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG	240
Qy	3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	3555
Db	241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA	300
Qy	3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT	3615
Db	301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT	360
Qy	3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTAG	3675
Db	361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTAG	420
Qy	3676 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	3735
Db	421 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	480
Qy	3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	3795
Db	481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	540
Qy	3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT	3855
Db	541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT	600
Qy	3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036 AGATCCTCCCCAGAGTCCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781 AGATCCTCCCCAGAGTCCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	4215
Db	901 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	960
Qy	4216 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275

Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCCTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCCTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTCTATTGGGTGACTTGGAGATTTATCTTTGTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTCTATTGGGTGACTTGGAGATTTATCTTTGTCTCT	1740
Qy	4995	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGT	5054
Db	1741	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACTTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAT	5174
Db	1861	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAT	1920

Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTCCTTGCCCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTCCTTGCCCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAA	2160
Qy	5415	GGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280
Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG	2340
Qy	5595	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400
Qy	5655	TAATGATCTTGCGTGGATCC	5674
Db	2401	TAATGATCTTGCGTGGATCC	2420

RESULT 12

US-11-067-064-81

; Sequence 81, Application US/11067064

; Publication No. US20050142144A1

; GENERAL INFORMATION:

; APPLICANT: SIMARD, John, J.L.

; APPLICANT: DIAMOND, David, C.

; APPLICANT: LIU, Zheng

; TITLE OF INVENTION: EPITOPE SEQUENCES

; FILE REFERENCE: MANNK.027C2

; CURRENT APPLICATION NUMBER: US/11/067,064

; CURRENT FILING DATE: 2005-02-25

; PRIOR APPLICATION NUMBER: US 60/282,211

; PRIOR FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: US 60/337,017

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: US 60/363,210

; PRIOR FILING DATE: 2002-03-07

; PRIOR APPLICATION NUMBER: US 10/117937

; PRIOR FILING DATE: 2002-04-04

; NUMBER OF SEQ ID NOS: 602

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 81

; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-067-064-81

Query Match 42.4%; Score 2408; DB 13; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db        1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db       61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          |||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTTCAGGTTTTTCAG 3675
          |||
Db      361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGACCAAGGAGAA 3735
          |||
Db      421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          |||
Db      481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 3855
          |||
Db      541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 600

Qy      3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
          |||
Db      601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy      3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
          |||
Db      661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy      3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035
          |||
Db      721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780
```

Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTGGAGATTTATCTTTGTTCTCT	4994

Db	1681		GTGTTCTCAGTAGTAGGTTTCTGTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	1740
Qy	4995		TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	5054
Db	1741		TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	1800
Qy	5055		TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801		TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115		TTTATT CAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861		TTTATT CAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175		AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921		AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235		TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981		TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295		ATGCATACCTGGATTTCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAA	5354
Db	2041		ATGCATACCTGGATTTCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAA	2100
Qy	5355		GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA	5414
Db	2101		GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA	2160
Qy	5415		GGCCCTGGGT TAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161		GGCCCTGGGT TAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475		G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221		G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280
Qy	5535		GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC AATG	5594
Db	2281		GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC AATG	2340
Qy	5595		CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341		CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400
Qy	5655		TAATGATCTTGGGTGGATCC	5674
Db	2401		TAATGATCTTGGGTGGATCC	2420

RESULT 13
 US-11-067-159-81
 ; Sequence 81, Application US/11067159
 ; Publication No. US20050221440A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SIMARD, John, J.L.
 ; APPLICANT: DIAMOND, David, C.
 ; APPLICANT: LIU, Zheng
 ; TITLE OF INVENTION: EPITOPE SEQUENCES

```

; FILE REFERENCE: MANNK.027C1
; CURRENT APPLICATION NUMBER: US/11/067,159
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 10/117937
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-067-159-81

```

```

Query Match          42.4%; Score 2408; DB 13; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

```

Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 3855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

```

Db	541	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT	600
Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500

Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTCTGTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTCTGTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	1740
Qy	4995	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	5054
Db	1741	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCTTGCCCTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCTTGCCCTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAC TGAGCATCTGCTTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAC TGAGCATCTGCTTTTTGGAA	2160
Qy	5415	GGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTTAGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221	G TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280
Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGCAATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGCAATG	2340
Qy	5595	CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400

Qy 5655 TAATGATCTTGGGTGGATCC 5674
|||||||
Db 2401 TAATGATCTTGGGTGGATCC 2420

RESULT 14

US-11-155-288-25

; Sequence 25, Application US/11155288

; Publication No. US20060008468A1

; GENERAL INFORMATION:

; APPLICANT: Chiang, Chih-Sheng

; APPLICANT: Simard, John J.L.

; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS

; FILE REFERENCE: MANNK.050A

; CURRENT APPLICATION NUMBER: US/11/155,288

; CURRENT FILING DATE: 2005-06-17

; PRIOR APPLICATION NUMBER: 60/580,969

; PRIOR FILING DATE: 2004-06-17

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 25

; LENGTH: 2420

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-155-288-25

Query Match 42.4%; Score 2408; DB 16; Length 2420;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
|||||||
Db 1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy 3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
|||||||
Db 61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy 3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
|||||||
Db 121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 180

Qy 3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
|||||||
Db 181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy 3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
|||||||
Db 241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy 3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
|||||||
Db 301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy 3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTCAGGTTTTTCAG 3675
|||||||
Db 361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTCAGGTTTTTCAG 420

Qy 3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAA 3735
|||||||

Db 421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy 3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
 |||

Db 481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy 3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 3855
 |||

Db 541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCT 600

Qy 3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
 |||

Db 601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy 3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCCTGGTGTGTGTGCAGGCTGCCAC 3975
 |||

Db 661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy 3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035
 |||

Db 721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780

Qy 4036 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 4095
 |||

Db 781 AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG 840

Qy 4096 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 4155
 |||

Db 841 ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG 900

Qy 4156 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT 4215
 |||

Db 901 TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT 960

Qy 4216 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 4275
 |||

Db 961 TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT 1020

Qy 4276 CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 4335
 |||

Db 1021 CATCAAAAATTACAAGCACTGTTTTCTTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA 1080

Qy 4336 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 4395
 |||

Db 1081 GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT 1140

Qy 4396 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 4455
 |||

Db 1141 CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC 1200

Qy 4456 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 4515
 |||

Db 1201 AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA 1260

Qy 4516 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 4575
 |||

Db 1261 GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA 1320

Qy 4576 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG 4634
 |||

Db 1321 TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG 1380

Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	1740
Qy	4995	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCTTGCGCTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCTTGCGCTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA	2160
Qy	5415	GGCCCTGGGTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG	5534
Db	2221	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG	2280

```

Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATG 5594
          |||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATG 2340

Qy      5595 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
          |||
Db      2341 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
          |||
Db      2401 TAATGATCTTGGGTGGATCC 2420

```

RESULT 15

US-10-093-766-41

; Sequence 41, Application US/10093766

; Publication No. US20030013099A1

; GENERAL INFORMATION:

; APPLICANT: Lasek, Amy W.

; APPLICANT: Jones, David A.

; APPLICANT: Karpf, Adam R.

; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS

; FILE REFERENCE: PA-0047 US

; CURRENT APPLICATION NUMBER: US/10/093,766

; CURRENT FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PERL Program

; SEQ ID NO 41

; LENGTH: 2420

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20030013099A1 410721.1

US-10-093-766-41

```

Query Match          42.4%;  Score 2404.8;  DB 6;  Length 2420;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 2417;  Conservative 0;  Mismatches 2;  Indels 1;  Gaps 1;

```

```

Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db      1   GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCACCCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61  ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCACCCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTCCTGGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTACACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCCTCAGGTACACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCTAGTCTCTAGTAAT 3615

```

Db	301	CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCTAGTCTCTAGTAAT	360
Qy	3616	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	3675
Db	361	CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	420
Qy	3676	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	3735
Db	421	GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA	480
Qy	3736	GATCTGTAAGTAGGCCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCCTCTCA	3795
Db	481	GATCTGTAAGTAGGCCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCCTCTCA	540
Qy	3796	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	3855
Db	541	CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	600
Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515

Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCT	1740
Qy	4995	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	5054
Db	1741	TTTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACGTAGCATCTGCTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACGTAGCATCTGCTTTTGGAA	2160

```

Qy      5415 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 5474
        |||
Db      2161 GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC 2220

Qy      5475 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 5534
        |||
Db      2221 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 2280

Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC AATG 5594
        |||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC AATG 2340

Qy      5595 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
        |||
Db      2341 CCCTGAGCTGGGGCATTTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
        |||
Db      2401 TAATGATCTTGGGTGGATCC 2420

```

Search completed: August 25, 2006, 15:22:13
Job time : 6187 secs

SCORE 1.3 BuildDate: 12/06/2005

SCORE Search Results Details for Application 08819669 and Search Result us-08-819-669e- 8.rnpbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 08819669 and Search Result us-08-819-669e-8.rnpbn.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2006, 13:39:22 ; Search time 856 Seconds
(without alignments)
10803.493 Million cell updates/sec

Title: US-08-819-669E-8
Perfect score: 5674
Sequence: 1 CCCGGGGCACCCTGGCATC.....TAATGATCTTGGGTGGATCC 5674

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2239192 seqs, 814926892 residues

Total number of hits satisfying chosen parameters: 4478384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq1:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5674	100.0	5674	8	US-11-253-240-8	Sequence 8, Appli
2	2419	42.6	2419	8	US-11-253-240-7	Sequence 7, Appli
3	2408	42.4	2420	9	US-11-323-049-18	Sequence 18, Appl
4	2408	42.4	2420	9	US-11-323-964-27	Sequence 27, Appl
5	2058.8	36.3	4157	8	US-11-253-240-9	Sequence 9, Appli
6	1762.6	31.1	4204	9	US-11-323-049-19	Sequence 19, Appl
7	1762.6	31.1	4204	9	US-11-323-964-28	Sequence 28, Appl
8	1678.8	29.6	2531	8	US-11-253-240-13	Sequence 13, Appl
9	1678.8	29.6	2531	8	US-11-253-240-14	Sequence 14, Appl
10	1504.6	26.5	2305	8	US-11-253-240-17	Sequence 17, Appl
11	1410.8	24.9	2226	8	US-11-253-240-16	Sequence 16, Appl
12	1188.2	20.9	1577	8	US-11-266-748A-87851	Sequence 87851, A
13	1188.2	20.9	1577	8	US-11-266-748A-112460	Sequence 112460,
c 14	1188.2	20.9	1577	8	US-11-266-748A-140662	Sequence 140662,
15	988.8	17.4	1640	8	US-11-253-240-11	Sequence 11, Appl
16	939.2	16.6	1000	8	US-11-266-748A-397184	Sequence 397184,
c 17	939.2	16.6	1000	8	US-11-266-748A-468230	Sequence 468230,
18	900.2	15.9	1810	8	US-11-253-240-20	Sequence 20, Appl
19	830.6	14.6	1947	8	US-11-253-240-19	Sequence 19, Appl
20	815.2	14.4	1412	8	US-11-253-240-21	Sequence 21, Appl
21	750.8	13.2	1068	8	US-11-253-240-15	Sequence 15, Appl
c 22	720.2	12.7	747	8	US-11-266-748A-212265	Sequence 212265,
23	699.6	12.3	1000	8	US-11-266-748A-286830	Sequence 286830,
c 24	699.6	12.3	1000	8	US-11-266-748A-338259	Sequence 338259,
25	647.8	11.4	942	8	US-11-266-748A-87853	Sequence 87853, A
26	647.8	11.4	942	8	US-11-266-748A-112462	Sequence 112462,
c 27	647.8	11.4	942	8	US-11-266-748A-140664	Sequence 140664,
28	646.6	11.4	1000	8	US-11-266-748A-284452	Sequence 284452,
c 29	646.6	11.4	1000	8	US-11-266-748A-335881	Sequence 335881,
30	646.6	11.4	1000	8	US-11-266-748A-394458	Sequence 394458,
c 31	646.6	11.4	1000	8	US-11-266-748A-465504	Sequence 465504,
32	634.4	11.2	1000	8	US-11-266-748A-290270	Sequence 290270,
c 33	634.4	11.2	1000	8	US-11-266-748A-341699	Sequence 341699,
34	634.4	11.2	1000	8	US-11-266-748A-401488	Sequence 401488,
c 35	634.4	11.2	1000	8	US-11-266-748A-472534	Sequence 472534,
36	633	11.2	1000	8	US-11-266-748A-221670	Sequence 221670,
37	633	11.2	1000	8	US-11-266-748A-397390	Sequence 397390,
c 38	633	11.2	1000	8	US-11-266-748A-468436	Sequence 468436,
39	627	11.1	1000	8	US-11-266-748A-405408	Sequence 405408,
c 40	627	11.1	1000	8	US-11-266-748A-476454	Sequence 476454,
41	583.4	10.3	1107	8	US-11-253-240-23	Sequence 23, Appl
42	567	10.0	1231	8	US-11-266-748A-87854	Sequence 87854, A
43	567	10.0	1231	8	US-11-266-748A-112463	Sequence 112463,
c 44	567	10.0	1231	8	US-11-266-748A-140665	Sequence 140665,
45	542.2	9.6	1200	8	US-11-266-748A-361126	Sequence 361126,

ALIGNMENTS

RESULT 1

US-11-253-240-8

; Sequence 8, Application US/11253240

; Publication No. US20060127356A1

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;

; van der Bruggen, Pierre; Boon-Falleur, Thierry

```

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/253,240
; FILING DATE: 17-Oct-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/579,543
; FILING DATE: 26-May-2000
; APPLICATION NUMBER: 09/583,850
; FILING DATE:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5674 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-1 gene
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-11-253-240-8

```

```

Query Match          100.0%;  Score 5674;  DB 8;  Length 5674;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5674;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

```

Qy      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCCGGGGCACCCTGGCATCCCTCCCCCTACCACCCCAATCCCTCCCTTTACGCCACCC 60

Qy      61 ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCCACCCCTG 120

```

Db	61		ATCCAAACATCTTCACGCTCACCCCCAGCCCAAGCCAGGCAGAATCCGGTTCACCCCTG	120
Qy	121		CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Db	121		CTCTCAACCCAGGGAAGCCAGGTGCCCAGATGTGACGCCACTGACTTGAGCATTAGTGG	180
Qy	181		TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Db	181		TTAGAGAGAAGCGAGGTTTTCGGTCTGAGGGGCGGCTTGAGATCGGTGGAGGGAAGCGGG	240
Qy	241		CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Db	241		CCCAGCTCTGTAAGGAGGCAAGGTGACATGCTGAGGGAGGACTGAGGACCCACTTACCCC	300
Qy	301		AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Db	301		AGATAGAGGACCCCAAATAATCCCTTCATGCCAGTCCTGGACCATCTGGTGGTGGACTTC	360
Qy	361		TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Db	361		TCAGGCTGGGCCACCCCCAGCCCCCTTGCTGCTTAAACCACTGGGGACTCGAAGTCAGAG	420
Qy	421		CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Db	421		CTCCGTGTGATCAGGGAAGGGCTGCTTAGGAGAGGGCAGCGTCCAGGCTCTGCCAGACAT	480
Qy	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Db	481		CATGCTCAGGATTCTCAAGGAGGGCTGAGGGTCCCTAAGACCCCACTCCCGTGACCCAAC	540
Qy	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Db	541		CCCCACTCCAATGCTCACTCCCGTGACCCAACCCCTCTTCATTGTCATTCCAACCCCCA	600
Qy	601		CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Db	601		CCCCACATCCCCACCCCATCCCTCAACCCTGATGCCCATCCGCCAGCCATTCCACCCT	660
Qy	661		CACCCCCACCCCCACCCCCACGCCCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Db	661		CACCCCCACCCCCACCCCCACGCCCCACTCCCACCCCCACCCAGGCAGGATCCGGTTCCCG	720
Qy	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Db	721		CCAGGAAACATCCGGGTGCCCGGATGTGACGCCACTGACTTGCGCATTGTGGGGCAGAGA	780
Qy	781		GAAGCGAGGTTTCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Db	781		GAAGCGAGGTTTCATTCTGAGGGACGGCGTAGAGTTCGGCCGAAGGAACCTGACCCAGG	840
Qy	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Db	841		CTCTGTGAGGAGGCAAGGTGAGAGGCTGAGGGAGGACTGAGGACCCCGCCACTCCAAATA	900
Qy	901		GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Db	901		GAGAGCCCCAAATATTCAGCCCCGCCCTTGCTGCCAGCCCTGGCCACCCGCGGGAAGA	960
Qy	961		CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTT	1020

Db	961	CGTCTCAGCCTGGGCTGCCCCCAGACCCCTGCTCCAAAAGCCTTGAGAGACACCAGGTTC	1020
Qy	1021	TTCTCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Db	1021	TTCTCCCAAGCTCTGGAATCAGAGGTTGCTGTGACCAGGGCAGGACTGGTTAGGAGAGG	1080
Qy	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Db	1081	GCAGGGCACAGGCTCTGCCAGGCATCAAGATCAGCACCCAAGAGGGAGGGCTGTGGGCCC	1140
Qy	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Db	1141	CCAAGACTGCACTCCAATCCCCACTCCCACCCATTTCGCATTCCCATCCCCACCCAACC	1200
Qy	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Db	1201	CCCATCTCCTCAGCTACACCTCCACCCCATCCCTACTCCTACTCCGTACCTGACCACC	1260
Qy	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCCTACTGCCCCAAC	1320
Db	1261	ACCCTCCAGCCCCAGCACCAGCCCCAACCCCTTCTGCCACCTCACCCCTACTGCCCCAAC	1320
Qy	1321	CCCACCCATCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTTCTGGCAGAATCC	1380
Db	1321	CCCACCCATCATCTCTCTCATGTGCCCCACTCCCATCGCCTCCCCCATTTCTGGCAGAATCC	1380
Qy	1381	GGTTTGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Db	1381	GGTTTGCCCTGCTCTCAACCCAGGGAAGCCCTGGTAGGCCCGATGTGAAACCACTGACT	1440
Qy	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCGAGGGGCGGCTTGAG	1500
Db	1441	TGAACCTCACAGATCTGAGAGAAGCCAGGTTTCAATTAATGGTTCGAGGGGCGGCTTGAG	1500
Qy	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Db	1501	ATCCACTGAGGGGAGTGGTTTTAGGCTCTGTGAGGAGGCAAGGTGAGATGCTGAGGGAGG	1560
Qy	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Db	1561	ACTGAGGAGGCACACACCCAGGTAGATGGCCCCAAAATGATCCAGTACCACCCCTGCTG	1620
Qy	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Db	1621	CCAGCCCTGGACCACCCGGCCAGGACAGATGTCTCAGCTGGACCACCCCGTCCCGTCC	1680
Qy	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Db	1681	CACTGCCACTTAACCCACAGGGCAATCTGTAGTCATAGCTTATGTGACCGGGGCAGGGTT	1740
Qy	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Db	1741	GGTCAGGAGAGGCAGGGCCAGGCATCAAGGTCCAGCATCCGCCCGGCATTAGGGTCAGG	1800
Qy	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Db	1801	ACCCTGGGAGGGAAC TGAGGGTTCCCCACCCACACCTGTCTCCTCATCTCCACCGCCACC	1860
Qy	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920
Db	1861	CCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGTGAGAATCCCTGCTG	1920

Qy	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Db	1921	TCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCACTCGGATCTTGACGTCCCCATCCA	1980
Qy	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Db	1981	GGGTCTGATGGAGGGAAGGGGCTTGAACAGGGCCTCAGGGGAGCAGAGGGAGGGCCCTAC	2040
Qy	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCTAGGACACCGACCCCTGTCTGAG	2100
Db	2041	TGCGAGATGAGGGAGGCCTCAGAGGACCCAGCACCCTAGGACACCGACCCCTGTCTGAG	2100
Qy	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Db	2101	ACTGAGGCTGCCACTTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGG	2160
Qy	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Db	2161	GTGGGACCCAGGCCTGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTT	2220
Qy	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Db	2221	GGAATCCAGATCAGTGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATG	2280
Qy	2281	GCCCATATTTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Db	2281	GCCCATATTTTCCTGCATCTTTGAGGTGACAGGACAGAGCTGTGGTCTGAGAAGTGGGGCC	2340
Qy	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Db	2341	TCAGGTCAACAGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATG	2400
Qy	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Db	2401	AGGACTGGGGATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCCTT	2460
Qy	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Db	2461	TTAGTAGCTCTAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCA	2520
Qy	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Db	2521	CAGGCAGGAAGTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCT	2580
Qy	2581	ACTCATGTCAGGGAATTGGGGGTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Db	2581	ACTCATGTCAGGGAATTGGGGGTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGT	2640
Qy	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTAGCCCTGGACACC	2700
Db	2641	GAGACAGACAAGGCTATTGGAATCCACACCCCAGAACCAAAGGGGTAGCCCTGGACACC	2700
Qy	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Db	2701	TCACCCAGGATGTGGCTTCTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCT	2760
Qy	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820
Db	2761	CATTCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCG	2820

Qy	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCAG	2880
Db	2821	GTCCCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCAG	2880
Qy	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCCAGAG	2940
Db	2881	GACCAGAACACTGAGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCCAGAG	2940
Qy	2941	AGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Db	2941	AGCATGGGCTGGGCCGCTGCGGAGGTCCTTCCGTTATCCTGGGATCATTGATGTCAGGG	3000
Qy	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Db	3001	ACGGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCC	3060
Qy	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Db	3061	CTGCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAAT	3120
Qy	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Db	3121	GAATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTT	3180
Qy	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTGGATTCTCAG	3240
Db	3181	GTCCCCTCCTGTCCTTCCATTCCCTTATCATGGATGTGAACTCTTGATTGGATTCTCAG	3240
Qy	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Db	3241	ACCAGCAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAA	3300
Qy	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Db	3301	CAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCTCCTG	3360
Qy	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Db	3361	GTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCCCT	3420
Qy	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Db	3421	CTTCCTGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTC	3480
Qy	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Db	3481	ACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAA	3540
Qy	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Db	3541	GGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTG	3600
Qy	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Db	3601	TCAGTCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCT	3660
Qy	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Db	3661	CCTTCAGGTTTTTCAGGGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAG	3720
Qy	3721	GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTC	3780

Db	3721		GAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTCAAGTCTC	3780
Qy	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Db	3781		AGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCT	3840
Qy	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Db	3841		CCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAG	3900
Qy	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Db	3901		TCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTG	3960
Qy	3961		TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCTGGAGGAGGTGCC	4020
Db	3961		TGTGCAGGCTGCCACCTCCTCCTCTCCTCTGGTCCTGGGCACCTGGAGGAGGTGCC	4020
Qy	4021		CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Db	4021		CACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTAC	4080
Qy	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Db	4081		CATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGG	4140
Qy	4141		GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Db	4141		GCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGC	4200
Qy	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Db	4201		TGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGA	4260
Qy	4261		AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Db	4261		AATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGC	4320
Qy	4321		CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Db	4321		CTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCA	4380
Qy	4381		CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Db	4381		CTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCA	4440
Qy	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Db	4441		GATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGG	4500
Qy	4501		CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Db	4501		CCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAG	4560
Qy	4561		GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Db	4561		GGAGCACAGTGCCATATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAA	4620
Qy	4621		GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGT	4680

Db	4621	GTACCTGGAGTACGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGT	4680
Qy	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Db	4681	CCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGT	4740
Qy	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Db	4741	GCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAG	4800
Qy	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Db	4801	GGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTT	4860
Qy	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Db	4861	CCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCT	4920
Qy	4921	GAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Db	4921	GAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATT	4980
Qy	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Db	4981	TATCTTTGTTCTCTTTTGGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC	5040
Qy	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Db	5041	TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTCGTGTATATAGTTTAAGGG	5100
Qy	5101	TAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT	5160
Db	5101	TAAGAGTCTTGTGTTTTATTCAGATTGGGAAATCCATTCTATTTGTGAATTGGGATAAT	5160
Qy	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Db	5161	AACAGCAGTGGAATAAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAA	5220
Qy	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Db	5221	AGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAA	5280
Qy	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Db	5281	ATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCTTCTTTGAGAATGTAAGAGAAAT	5340
Qy	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Db	5341	TAAATCTGAATAAAGAATTCTTCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCA	5400
Qy	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Db	5401	TCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATAC	5460
Qy	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Db	5461	CCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTC	5520
Qy	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGAGGGCTCCGGGTGAGAGTG	5580
Db	5521	CTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGGTGAGGGCTCCGGGTGAGAGTG	5580

```

Qy      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640
          |||
Db      5581 GTGGAGTGTCAATGCCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCT 5640

Qy      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674
          |||
Db      5641 GGGGGAGCTGATTGTAATGATCTTGGGTGGATCC 5674

```

RESULT 2

US-11-253-240-7

```

; Sequence 7, Application US/11253240
; Publication No. US20060127356A1
; GENERAL INFORMATION:
; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;
;           van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
;                   Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/253,240
; FILING DATE: 17-Oct-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/579,543
; FILING DATE: 26-May-2000
; APPLICATION NUMBER: 09/583,850
; FILING DATE:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2419 base pairs
; TYPE: nucleic acid

```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-11-253-240-7
```

```
Query Match          42.6%; Score 2419; DB 8; Length 2419;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db        1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db        61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 3435
          |||
Db       121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db       181 GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db       241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          |||
Db       301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 3675
          |||
Db       361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG 420

Qy      3676 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 3735
          |||
Db       421 GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          |||
Db       481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 3855
          |||
Db       541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 600

Qy      3856 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 3915
          |||
Db       601 GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC 660

Qy      3916 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 3975
          |||
Db       661 TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC 720

Qy      3976 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 4035
          |||
Db       721 CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC 780
```

Qy	4036	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCCTACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGCTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGCTCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	4635
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGG	1380
Qy	4636	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	4695
Db	1381	CAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCT	1440
Qy	4696	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGCTTT	4755
Db	1441	GAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGCTTT	1500
Qy	4756	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	4815
Db	1501	TTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGA	1560
Qy	4816	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	4875
Db	1561	GTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCA	1620
Qy	4876	GCAGCTTCCCTGCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	4935
Db	1621	GCAGCTTCCCTGCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCAG	1680

Qy	4936	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	4995
Db	1681	TGTTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTT	1740
Qy	4996	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTT	5055
Db	1741	TTGGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTT	1800
Qy	5056	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTTGTT	5115
Db	1801	TATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTTGTT	1860
Qy	5116	TTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA	5175
Db	1861	TTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAATA	1920
Qy	5176	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	5235
Db	1921	AGTACTTAGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATT	1980
Qy	5236	AAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	5295
Db	1981	AAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATA	2040
Qy	5296	TGCATACCTGGATTTCCTTGCCCTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAG	5355
Db	2041	TGCATACCTGGATTTCCTTGCCCTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAG	2100
Qy	5356	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGGAAG	5415
Db	2101	AATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGGAAG	2160
Qy	5416	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	5475
Db	2161	GCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCG	2220
Qy	5476	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	5535
Db	2221	TAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGG	2280
Qy	5536	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATGC	5595
Db	2281	GAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATGC	2340
Qy	5596	CCTGAGCTGGGGCATT TTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	5655
Db	2341	CCTGAGCTGGGGCATT TTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTGT	2400
Qy	5656	AATGATCTTGGGTGGATCC	5674
Db	2401	AATGATCTTGGGTGGATCC	2419

RESULT 3

US-11-323-049-18

; Sequence 18, Application US/11323049

; Publication No. US2006015969A1

; GENERAL INFORMATION:

; APPLICANT: Chiang, Chih-Sheng

; APPLICANT: Simard, John J.L.

; APPLICANT: Diamond, David C.

```

; APPLICANT: Bot, Adrian Ion
; APPLICANT: Liu , Xiping
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.049A
; CURRENT APPLICATION NUMBER: US/11/323,049
; CURRENT FILING DATE: 2005-12-29
; PRIOR APPLICATION NUMBER: 60/640,598
; PRIOR FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-323-049-18

```

```

Query Match          42.4%; Score 2408; DB 9; Length 2420;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

```

Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db      1 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 3615
          |||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTCAG 3675
          |||
Db      361 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTCAG 420

Qy      3676 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGACCAAGGAGAA 3735
          |||
Db      421 GGGACAGGCCAAGCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGACCAAGGAGAA 480

Qy      3736 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 3795
          |||
Db      481 GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA 540

Qy      3796 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 3855
          |||
Db      541 CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT 600

```

Qy	3856	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601	GCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661	TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721	CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036	AGATCCTCCCCAGAGTCCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781	AGATCCTCCCCAGAGTCCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841	ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	4215
Db	901	TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTT	960
Qy	4216	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961	TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021	CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081	GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141	CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201	AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575
Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814

Db	1501		1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTTCATTGGGTGACTTGGAGATTTATCTTTGTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTTCATTGGGTGACTTGGAGATTTATCTTTGTCTCT	1740
Qy	4995	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	5054
Db	1741	TTTGAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	5174
Db	1861	TTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAAAT	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCTTGCGCTCTTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCTTGCGCTCTTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA	2160
Qy	5415	GGCCCTGGGTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220
Qy	5475	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	5534
Db	2221	GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAG	2280
Qy	5535	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC AATG	5594
Db	2281	GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC AATG	2340
Qy	5595	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	5654
Db	2341	CCCTGAGCTGGGGCATTTTGGGCTTTGGGAACTGCAGTTCCTTCTGGGGGAGCTGATTG	2400
Qy	5655	TAATGATCTTGGGTGGATCC	5674

Db 2401 TAATGATCTTGGGTGGATCC 2420

RESULT 4

US-11-323-964-27

; Sequence 27, Application US/11323964

; Publication No. US20060159689A1

; GENERAL INFORMATION:

; APPLICANT: Chiang, Chih-Sheng

; APPLICANT: Simard, John J.L.

; APPLICANT: Diamond, David C.

; APPLICANT: Bot, Adrian Ion

; APPLICANT: Liu, Xiping

; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS

; FILE REFERENCE: MANNK.050CP1

; CURRENT APPLICATION NUMBER: US/11/323,964

; CURRENT FILING DATE: 2005-12-29

; PRIOR APPLICATION NUMBER: 11/155,288

; PRIOR FILING DATE: 2005-06-17

; PRIOR APPLICATION NUMBER: PCT/US2005/021836

; PRIOR FILING DATE: 2005-06-17

; PRIOR APPLICATION NUMBER: 60/580,969

; PRIOR FILING DATE: 2004-06-17

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 27

; LENGTH: 2420

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-323-964-27

Query Match 42.4%; Score 2408; DB 9; Length 2420;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2419; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||
Db      1  GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61  ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          |||
Db      121 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||
Db      181 GGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||
Db      241 CACAGGGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 3615
          |||
Db      301 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCCTGTAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTCAGGTTTTCAG 3675
```

Db	361		CGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTTTTTCAG	420
Qy	3676		GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACC AAGGAGAA	3735
Db	421		GGGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACC AAGGAGAA	480
Qy	3736		GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	3795
Db	481		GATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTTTCAGTTCTCAGCTGAGGCCTCTCA	540
Qy	3796		CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	3855
Db	541		CACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCCT	600
Qy	3856		GCCTGCTGCCCCGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	3915
Db	601		GCCTGCTGCCCCGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCC	660
Qy	3916		TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	3975
Db	661		TGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCAC	720
Qy	3976		CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	4035
Db	721		CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAAC	780
Qy	4036		AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	4095
Db	781		AGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCG	840
Qy	4096		ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	4155
Db	841		ACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTG	900
Qy	4156		TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	4215
Db	901		TATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTT	960
Qy	4216		TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	4275
Db	961		TCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGT	1020
Qy	4276		CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	4335
Db	1021		CATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGCA	1080
Qy	4336		GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	4395
Db	1081		GCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCCTTGT	1140
Qy	4396		CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	4455
Db	1141		CACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGAC	1200
Qy	4456		AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	4515
Db	1201		AGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGA	1260
Qy	4516		GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	4575

Db	1261	GGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTA	1320
Qy	4576	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CG	4634
Db	1321	TGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCG	1380
Qy	4635	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	4694
Db	1381	GCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGC	1440
Qy	4695	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	4754
Db	1441	TGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTT	1500
Qy	4755	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	4814
Db	1501	TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATG	1560
Qy	4815	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	4874
Db	1561	AGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCC	1620
Qy	4875	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	4934
Db	1621	AGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCATTCTTCACTCTGAAGAGAGCGGTCA	1680
Qy	4935	GTGTTCTCAGTAGTAGGTTTCTGTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	4994
Db	1681	GTGTTCTCAGTAGTAGGTTTCTGTCTATTGGGTGACTTGGAGATTATCTTTGTTCTCT	1740
Qy	4995	TTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	5054
Db	1741	TTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGT	1800
Qy	5055	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	5114
Db	1801	TTATGAATGACAGCAGTCACACAGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGT	1860
Qy	5115	TTTATT CAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAA	5174
Db	1861	TTTATT CAGATTGGGAAATCCATTCTATTTTGTGAATTGGGATAATAACAGCAGTGGAA	1920
Qy	5175	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	5234
Db	1921	AAGTACTTAGAAATGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAACTAAAGAAAT	1980
Qy	5235	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	5294
Db	1981	TAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATAT	2040
Qy	5295	ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	5354
Db	2041	ATGCATACCTGGATTTCCCTTGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAA	2100
Qy	5355	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA	5414
Db	2101	GAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTGGAA	2160
Qy	5415	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	5474
Db	2161	GGCCCTGGGTTAGTAGTGGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTC	2220

```

Qy      5475 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 5534
          |||
Db      2221 GTAGAGTCTAGGAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAG 2280

Qy      5535 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 5594
          |||
Db      2281 GGAAAAGTGAGAGAGGGGTGAGGGTGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATG 2340

Qy      5595 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 5654
          |||
Db      2341 CCCTGAGCTGGGGCATT TTTGGGCTTTGGGAAACTGCAGTTCCTTCTGGGGGAGCTGATTG 2400

Qy      5655 TAATGATCTTGGGTGGATCC 5674
          |||
Db      2401 TAATGATCTTGGGTGGATCC 2420

```

RESULT 5

US-11-253-240-9

; Sequence 9, Application US/11253240

; Publication No. US20060127356A1

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;
; van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felte & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/11/253,240
; FILING DATE: 17-Oct-2005
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/579,543
; FILING DATE: 26-May-2000
; APPLICATION NUMBER: 09/583,850
; FILING DATE:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946

```

;          REFERENCE/DOCKET NUMBER: LUD 5353
;          TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (212) 688-9200
;          TELEFAX: (212) 838-3884
;          INFORMATION FOR SEQ ID NO: 9:
;          SEQUENCE CHARACTERISTICS:
;          LENGTH: 4157 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;          MOLECULE TYPE: genomic DNA
;          FEATURE:
;          NAME/KEY:     MAGE-2 gene
;          SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-11-253-240-9

```

```

Query Match          36.3%;   Score 2058.8;   DB 8;   Length 4157;
Best Local Similarity 75.3%;   Pred. No. 0;
Matches 3172;   Conservative    0;   Mismatches 837;   Indels 201;   Gaps 41;

```

```

Qy      1351 CCCATCGCCTCCCCCATCTTGGCAGAATCCGGTT-TGCCCCTGCTCTCAACCCAGGGAAG 1409
          |||||  |||||  | ||||| ||||| || || || ||||| |||||
Db      1   CCCATCCAGATCCCCATCCGGGCAGAATCCGGTTCCACCCTTGCCGTGAACCCAGGGAAG 60

Qy      1410 CCCTGGTAGGCCCGATGTGAAACCACTGACTTGAACCTCACAGATCTGAGAGAAGCCAGG 1469
          | || | || |||||  ||||| || || | || || || || || ||
Db      61 TCACGG--GCCCGGATGTGACGCCACTGACTTGACATTGGAGGTCAGAGGACAGCGAGA 118

Qy      1470 TTCATTTAATGGTTCTGAGGGGCGGCTTGAGATCCACTGAGGGGAGTGGTTTATAGGCTCT 1529
          |||  | | |||||  |||| || || | |||| || | |||||
Db      119 TTC-----TCGCCCTGAGCAACGGCCTGACGTCGGCGGAGGGAAGCAGGCGCAGGCTCC 172

Qy      1530 GTGAGGAGGCAAGGTGAGATGCTGAGGGAGGACTGAGGAGGCACACACCCAGGTTAGATG 1589
          ||||| ||||| || || ||||| ||||| || || ||||| || || ||
Db      173 GTGAGGAGGCAAGGTAAGACGCCGAGGGAGGACTGAGGCGGGCCTCACCCAGACAGAGG 232

Qy      1590 GCCCCAAATGATCCAGTACCACCCCTGCTGCCAGCCCTGGACCACCCGGCCAGGACAGA 1649
          ||||| || | |||||  | || ||||| || ||||| ||||| || || |||
Db      233 GCCCCCAATTAATCCAGCGCTGCCTCTGCTGCCGGGCTGGACCACCTGCAGGGGAAGA 292

Qy      1650 TGTCTCAG-----CTGGACCACCCCCCGTCCCGTCCCACTGCCACTTAACCCACAGGG 1702
          |||||  |||||  | | | | || | || | || | || |||||
Db      293 CTTCTCAGGCTCAGTCGCCACCACCTCACCCGCCACCCCGCCGCTTTAACCGCAGGG 352

Qy      1703 CAATCTGTAGTCATAGCTTA-TGTGACCGGGGCAGGGTTGGTCAGGAGAGGCAGGGCCCA 1761
          | ||||  || | |||||  ||||| ||||| |||| || || || |
Db      353 AACTCTGGCGTAAGAGCTTTGTGTGACCAGGGCAGGGCTGGTTAGAAGTGC----- 403

Qy      1762 GGCATCAAGGTCCAGCATCCGCCCCGATTAGGGTCAGGACCCTGGGAGGGAAGTGAAGG 1821
          ||| || ||||  || || || || | ||||| ||||| ||||| |||||
Db      404 ----TCAGGGCCCAGACTCAGCCAGGAATCAAGGTGAGGACCCCAAGAGGGGACTGAGGG 459

Qy      1822 TTCCCCACCCACACCTGTCTCCTCATCTCC----- 1851
          ||||| || | || | | |||
Db      460 CAACCCACCCCTACCCTCACTACCAATCCCATCCCCAACACCAACCCACCCCATCC 519

Qy      1852 -----ACCGCCACCCCACTCACATTCCCATACCTACCCCTACCCCAACCTCATCTTGT 1906
          || | |||||  || || || | | || || || || || || || ||
Db      520 CTCAAACACCAACCCACCCCAAAACCCATTCCCATCTCCTCCCCACCACCATCTGG 579

Qy      1907 CAGAAT-----CCCTGCTGTCAACCCACGGAAGCCACGGGAATGGCGGCCAGGCA 1956

```

Db	580	CAGAATCCGGCTTTGCCCCGTGCAATCAACCCACGGAAGCTCCGGGAATGGCGGCCAAGCA	639
Qy	1957	CTCGGATCTTGACGTCCCCATCCAGGGTCTGATGGAGGGAAGGGG-----CTTGAAC	2008
Db	640	CGCGGATCCTGACGTTACATGTACGG-CTAAGGGAGGGAAGGGGTGGGTCTCGTGAGT	698
Qy	2009	AGGGCCTCAGGGGAGCAGAGGGAGGGC-----CCTACTGCGAGATGAGGGAGGCCTCAGA	2063
Db	699	ATGGCCTTTGGGATGCAGAGGAAGGGCCAGGCCTCCTGGAAGACAGTGGAGTCCCTTAGG	758
Qy	2064	GGACCCAGCACCCTAGGA-----CACCGCACCCCTGTCTGAGACTGAGGCTGCCAC	2114
Db	759	GGACCCAGCATGCCAGGACAGGGGGCCACTGTACCCCTGTCTCAAAC TGAGCCACCTTT	818
Qy	2115	TTCTGGCCTCAAGAATCAGAACGATGGGGACTCAGATTGCATGGGGGTGGGACCCAGGCC	2174
Db	819	TCATTACGCCGAGGGAATCCTAGGGATGCAGACCCACTTCAGGGGGTTGGGGCCAGCCT	878
Qy	2175	TGCAAGGCTTACGCGGAGGAAGAGGAGGGAGGACTCAGGGGACCTTGAATCCAGATCAG	2234
Db	879	GCGAGGAGTCAAGGGGAGGAAGAAGAGGGAGGACTGAGGGGACCTTGGAGTCCAGATCAG	938
Qy	2235	TGTGGACCTCGGCCCTGAGAGGTCCAGGGCACGGTGGCCACATATGGCCCATATTTCTCTG	2294
Db	939	TGGCAACCTTGG-GCTGGGGGATCCTGGGCACAGTGGCCGAATGTGCCCGTGCTCATTG	997
Qy	2295	CATCTTTGAGGTGAC----AGGACAGAGCTGTGGTCTGAGAAGTGGGGCCTCAGGTCAAC	2350
Db	998	CACCTTCAGGGTGACAGAGAGTTGAGGGCTGTGGTCTGAGGGCTGGGACTTCAGGTACAGC	1057
Qy	2351	AGAGGGAGGAGTTCCAGGATCCATATGGCCCAAGATGTGCCCCCTTCATGAGGACTGGGG	2410
Db	1058	AGAGGGAGGAATCCCAGGATCTGCCGGACCCAAGGTGTGCCCCCTTCATGAGGACTCCCC	1117
Qy	2411	ATATCCCCGGCTCAGAAAGAAGGGACTCCACACAGTCTGGCTGTCCCTTTTAGTAGCTC	2470
Db	1118	ATACCCCCGGCCCAGAAAGAAGGGATGCCACAGAGTCTGGAAGTAAATTGTTCTTAGCTC	1177
Qy	2471	TAGGGGGACCAGATCAGGGATGGCGGTATGTTCCATTCTCACTTGTACCACAGGCAGGAA	2530
Db	1178	TGGGGGAACCTGATCAGGGATGGCCCTAAGTGACAATCTCATTGTGTACCACAGGCAGGAG	1237
Qy	2531	GTTGGGGGGCCCTCAGGGAGATGGGGTCTTGGGGTAAAGGGGGGATGTCTACTCATGTCA	2590
Db	1238	GTTGGGGAAACCTCAGGGAGATAAGGTGTTGGTGTAAAGAGGAGCTGTCTGCTCATTTC	1297
Qy	2591	GGGAATTGGGGGTGAGGAAGCACAGGCGCTGGCAGGAATAAAGATGAGTGAGACAGACA	2650
Db	1298	GGGGGTTCCCCCCTTGAGAAAGGGCAGTCCCTGGCAGGAGTAAAGATGAGTAACCCACAGG	1357
Qy	2651	AGGCTATTGGAATCCACACCCCAAGAAAGGGGTAGCCCTGGACACCTCACCCAGGA	2710
Db	1358	AGGCCATCATAACGTTACCCCTAGAACCAAGGGGTAGCCCTGGACAACGCACGTGGGG	1417
Qy	2711	T-----GTGGCTTCTTTTTTCACTCCTGTTTCCAGATCTGGGGCAGGTGAGGACCTCAT	2763
Db	1418	TAACAGGATGTGGCCCCCTCCTCACTTGTCTTTCCAGATCTCAGGGAGTTGATGACCTTGT	1477
Qy	2764	TCTCAGAGGGTGACTCAGGTCAACGTAGGGACCCCCATCTGGTCTAAAGACAGAGCGGTC	2823

Db	1478	TTTCAGAAGGTGACTCAGTCAACACAGGGG---CCCCTCTGGTTCGACAGATGCAGTGGTT	1534
Qy	2824	CCAGGATCTGCCATGCGTTTCGGGTGAGGAACATGAGGGAGGACTGAGGGTACCCCAGGAC	2883
Db	1535	CTAGGATCTGCCAAGCATCCAGGTGGAGAGCCTGAGGTAGGATTGAGGGTACCCTGGGC	1594
Qy	2884	CAGAACACTG-AGGGAGACTGCACAGAAATCAGCCCTGCCCCTGCTGTCACCCAGAGAG	2942
Db	1595	CAGAAATGCAGCAAGGGGGCCCCATAGAAATCTGCCCTGCCCCTGCGGTTACTTCAGAGAC	1654
Qy	2943	CATGGGCTGGGCCGTCTGCCGAGGTCTTCCGTTATCCTGGGATCATTGATGTCAGGGAC	3002
Db	1655	CCTGGGCAGGGCTGTCTAGCTGAAGTCCCTCCATTAT-CTGGGATCTTTGATGTCAGGGAA	1713
Qy	3003	GGGGAGGCCCTTGGTCTGAGAAGGCTGCGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCCCT	3062
Db	1714	GGGGAGGCCCTTGGTCTGAGAAGGGCTGGAGTCAGGTCAGTAGAGGGAGGGTCTCAGGCCCT	1773
Qy	3063	GCCAGGAGTCAAGGTGAGGACCAAGCGGGCACCTCACCCAGGACACATTAATTCCAATGA	3122
Db	1774	GCCAGGAGTGGACGTGAGGACCAAGCGGACTCGTCACCCAGGACACCTGGACTCCAATGA	1833
Qy	3123	ATTTTGATATCTCTTGCTGCCCTTCCCCAAGGACCTAGGCACGTGTGGCCAGATGTTTGT	3182
Db	1834	A-TTTGACATCTCTCGTTGTCTTTCGCGGAGGACCTGGTACGTATGGCCAGATGTGGGT	1892
Qy	3183	CCCCTC-CTGTCTTCCATTCCCTTATCATGGATGTGAACTCTTG--ATTTGGATTTCTCA	3239
Db	1893	CCCCTCTATCTCTTCTGTACCATATCAGGGATGTGAGTTCTTGACATGAGAGATTCTCA	1952
Qy	3240	GACCAGCAAAAAGGGCAGGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGA	3299
Db	1953	AGCCAGCAAAAAGGGTGGGAT-TAGGCCCTACAAGGAGAAAGGTGAGGGCCCTGAGTGAGC	2011
Qy	3300	ACAGAGGGGGTCATCCACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCT	3359
Db	2012	ACAGAGGGGACCCTCCACCCAAGTAGAGTGGGGACCTCACGGAGTCTGGCCAACCCTGCT	2071
Qy	3360	GGTAGCACTGAGAAGCCAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCC	3419
Db	2072	GAGACTTCTGGGAATCCGTGGCTGTGCTTGCACTCTGCACACTGAAGGCCCGTGCATTCC	2131
Qy	3420	TCTTCCT-----GGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATC	3472
Db	2132	TCTCCCAGGAATCAGGAGCTCCAGGAACCAGGCAGTGAGGCCTTGGTCTGAGTCAGT-GC	2190
Qy	3473	CTCAGGTCACAGAGCAGAGGATGCACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATG	3532
Db	2191	CTCAGGTCACAGAGCAGAGGGGACGCAGACAGTGCCAACACTGAAGGTTTGCCCTGGAATG	2250
Qy	3533	CACACCAAGGGCCCCACCTGCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCA-CC	3591
Db	2251	CACACCAAGGGCCCCACCCGCC-CAGAACAAATGGGACTCCAGAGGGCCTGGCCTCACCC	2309
Qy	3592	TCCCTACTGTCTAGTCCCTGTAGAATCGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCT	3650
Db	2310	TCCCTATTCTCAGTCCCTGCAGCCTGAGCATGTGCTGGCCGGCTGTACCCTGAGGTGCCCT	2369
Qy	3651	CTCACTTCCTCCTTCAGGTTTTTCA-GGGGACAGGCCAACCCAGAGGACAGGATTCCCTGG	3709
Db	2370	CCCACTTCCTCCTTCAGGTTCTGAGGGGGACAGGCTGACAAGTAGGACCCGAGGCACTGG	2429

Qy	3710	AGGCCACAGAGGAGCACCAAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAG	3769
Db	2430	AGGAGCATTG-----AAGGAGAAGATCTGTAAGTAAGCCTTTGTCAGAGCCTCCAAG	2481
Qy	3770	GTTTCAG-----TTCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGG	3824
Db	2482	GTTTCAGTTTCAGTTCTCACCTAAGGCCTCACACACGCTCCTTCTCTCCCCAGGCCTGTGGG	2541
Qy	3825	TCTTCATTGCCCAGCTCCTGCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGT	3884
Db	2542	TCTTCATTGCCCAGCTCCTGCCCGCACTCCTGCCTGCTGCCCTGACCAGAGTCATCATGC	2601
Qy	3885	CTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGG	3944
Db	2602	CTCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCTTGAGGCCCGAGGAGAGG	2661
Qy	3945	CCCTGGGCCTGGTGTGTGTGCAGGCT-----GCCACCTCCTCCT	3983
Db	2662	CCCTGGGCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGCAGACCGCTTCTTCCT	2721
Qy	3984	CCTCTCCTCTGGTCTTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAACAGATCCTC	4043
Db	2722	CTTCTACTCTAGTGGAAGTTACCCCTGGGGGAGGTGCCTGCTGCCGACTCACCGAGTCCTC	2781
Qy	4044	CCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGC	4103
Db	2782	CCCACAGTCCTCAGGGAGCCTCCAGCTTCTCGACTACCATCAACTTACACTCTTTGGAGAC	2841
Qy	4104	AACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGATCCTGG	4163
Db	2842	AATCCGATGAGGGCTCCAGCAACCAAGAAGAGGAGGGGCCAAGAATGTTCCCGACCTGG	2901
Qy	4164	AGTCCTTGTTCCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCC	4223
Db	2902	AGTCCGAGTTCCAAGCAGCAATCAGTAGGAAGATGGTTGAGTTGGTTTCATTTCTGCTCC	2961
Qy	4224	TCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAA	4283
Db	2962	TCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGAGAGTGTCTCAGAA	3021
Qy	4284	ATTACAAGCACTGTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCT	4343
Db	3022	ATTGCCAGGACTTCTTTCCCGTGATCTTCAGCAAAGCCTCCGAGTACTTGACGCTGGTCT	3081
Qy	4344	TTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGTACCTGCC	4403
Db	3082	TTGGCATCGAGGTGGTGAAGTGGTCCCCATCAGCCACTTGTACATCCTTGTACCTGCC	3141
Qy	4404	TAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCC	4463
Db	3142	TGGGCCTCTCCTACGATGGCCTGCTGGGCGACAATCAGGTCATGCCCAAGACAGGCCTCC	3201
Qy	4464	TGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCT	4523
Db	3202	TGATAATCGTCCTGGCCATAATCGCAATAGAGGGCGACTGTGCCCTGAGGAGAAAATCT	3261
Qy	4524	GGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGC	4583
Db	3262	GGGAGGAGCTGAGTATGTTGGAGGTGTTGAGGGGAGGGAGGACAGTGTCTTCGCACATC	3321

Qy	4584	CCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGC	4642
Db	3322	CCAGGAAGCTGCTCATGCAAGATCTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGC	3381
Qy	4643	CGGACAGTGATCCCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCTGAAACCA	4702
Db	3382	CCGGCAGTGATCCTGCATGCTACGAGTTCTGTGGGGTCCAAGGGCCCTCATTGAAACCA	3441
Qy	4703	GCTATGTGAAAGTCCCTTGAGTATGTGATCAAGGTCAGTGCAGAGTTCGCTTTTTCTTCC	4762
Db	3442	GCTATGTGAAAGTCCCTGCACCATACTAAAGATCGGTGGAGAACCTCACATTTCTTACC	3501
Qy	4763	CATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAG	4822
Db	3502	CACCCCTGCATGAACGGGCTTTGAGAGAGGGAGAAGAGTGAGTCTCAGCACATGTTGCAG	3561
Qy	4823	CCAAGGCCAGTGGGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTT	4882
Db	3562	CCAGGGCCAGTGGGAGGGGGTCTGGGCCAGTGCACCTTCCAGGGCCCATCCATTAGCTT	3621
Qy	4883	CCCCTGCCTCGTGTGACATGAGGCCCATTTCTT--CACTCTGAAGAGAGCGGTGAGTTTC	4940
Db	3622	CCACTGCCTCGTGTGATATGAGGCCCATTCCTGCCTCTTTGAAGAGAGCAGTCAGCATTC	3681
Qy	4941	TCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTCTCTTTTGG	5000
Db	3682	TTAGCAGTGAGTTTCTGTTCTGTTGGATGACTTTGAGATTTATCTTTCTTTCTGTTGG	3741
Qy	5001	ATTGTTCAAATGTTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTTTATGA	5060
Db	3742	ATTGTTCAAATG-TTCCTTTTAACAAATGGTTGGATGAAC TTCAGCATCCAAGTTTATGA	3800
Qy	5061	ATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTA	5118
Db	3801	ATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGGTAAGAGTCTTGTGTTTTA	3860
Qy	5119	TTCAGATTGGGAAATCCATTCTATTTGTGAATTG--GGATAATAACAGCAGTGGAATAA	5176
Db	3861	TTCAGATTGGGAAATCCATTCCATTTGTGAGTTGTACATAATAACAGCAGTGGAATAT	3920
Qy	5177	GTACTTAGAAAATGT---GAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAA	5232
Db	3921	GTATTGCGCTATATTGTGAACGAATTAGCAGTAAAATACATGATACAAGGAAC-----	3973
Qy	5233	ATTAAGAGATAGTCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAAATTTTAAAGAT	5292
Db	3974	-TCAAAAGATAGTTAATTCTTGCCCTTATACCTCAGTCTATTATGTAAAA---TTAAAAAT	4029
Qy	5293	ATATGCATACCTGGATTTCCTTGCGCTCTTTGAGAATGTAAGAGAAATTAAATCTGAATA	5352
Db	4030	ATGTGTA-----TGTTTTGCTTCTTTGAGAATGCAAAGAAATTAAATCTGAATA	4080
Qy	5353	AAGAATTCTTCCTGTTCACTGGCTCTTTTCTTCTCCATGCAC TGAGCATCTGCTTTTTGG	5412
Db	4081	---AATTCTTCCTGTTCACTGGCTCATTTCTTTACCATTCACTCAGCATCTGCTCTGTGG	4137
Qy	5413	AAGGCCCTGG	5422
Db	4138	AAGGCCCTGG	4147

1 1

—

http://es/ScoreAccessWeb/GetItem.action?AppId=08819669&seqId=609520&ItemName=us... 8/30/06

Qy	3266	CCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGAG	3325
Db	1844	CCTATAAGGAGAAAGGTGAGGGCCCTGAGTGAGCACAGAGGGGATCCTCCACCCAGTAG	1903
Qy	3326	AGTGGGGATGTCACAGAGTCCAGCCCACCTCCTGGTAGCACTGAGAAGCCAGGGCTGTG	3385
Db	1904	AGTGGGGACCTCACAGAGTCTGGCCAACCTCCTGACAGTTCTGGGAATCCGTGGCTGCG	1963
Qy	3386	CTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTC-----CTGGAGCTCCAGGA	3438
Db	1964	TTTGCTGTCTGCACATTGGGGGGCCCGTGGATTCTCTCTCCAGGAATCAGGAGCTCCAGGA	2023
Qy	3439	ACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCAC	3498
Db	2024	ACAAGGCAGTGAGGACTTGGTCTGAGGCAGTGTCTCAGGTCACAGAGTAGAGGGGGCTC	2083
Qy	3499	AGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAG	3558
Db	2084	AGATAGTGCCAACGGTGAAGGTTTGCTTGGATTCAAACCAAGGGCCCCACCTGCCCCAG	2143
Qy	3559	GACACATAGGACTCCACAGAGTCTGGCCTCA-CCTCCCTACTGTCAGTCTGTAGAATCG	3617
Db	2144	AACACAT-GGACTCCAGAGCGCCTGGCCTCACCTCAATACTTTCAGTCTGCAGCCTCA	2202
Qy	3618	ACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTTCAGGTTTTCAGG	3676
Db	2203	GCATGCGCTGGCCGGATGTACCCTGAGGTGCCCTCTCACTTCCTCCTTCAGGTTCTGAGG	2262
Qy	3677	GGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAGGAGAAG	3736
Db	2263	GGACAGGCTGACCTGGAGGACCAGAGGCCCCCGAGGAGCACTG-----AAGGAGAAG	2315
Qy	3737	ATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGG-----TTCAGTTCTCAGCTGAGGCCT	3791
Db	2316	ATCTGTAAGTAAGCCTTTGTTAGAGCCTCCAAGGTTCCATTTCAGTACTCAGCTGAGGTCT	2375
Qy	3792	CTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCCACAC	3851
Db	2376	CTCACATGCTCCCTCTCTCCCCAGGCCAGTGGGTCTCCATTGCCCAGCTCCTGCCCCACAC	2435
Qy	3852	TCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCA	3911
Db	2436	TCCCGCCTGTTGCCCTGACCAGAGTCATCATGCCTCTTGAGCAGAGGAGTCAGCACTGCA	2495
Qy	3912	AGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCT-	3970
Db	2496	AGCCTGAAGAAGGCCCTTGAGGCCCGAGGAGAGGCCCTGGGCCTGGTGGGTGCGCAGGCTC	2555
Qy	3971	-----GCCACCTCCTCCTCCTCCTCCTGCTGCTGGGCACCCCTGG	4010
Db	2556	CTGCTACTGAGGAGCAGGAGGCTGCCTCCTCCTCTTCTACTCTAGTTGAAGTCACCCTGG	2615
Qy	4011	AGGAGGTGCCCAGTCTGGGTCAACAGATCCTCCCCAGAGTCTCAGGGAGCCTCCGCCT	4070
Db	2616	GGGAGGTGCCCTGCTGCCGAGTCACCAGATCCTCCCCAGAGTCTCAGGGAGCCTCCAGCC	2675
Qy	4071	TTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTG	4130
Db	2676	TCCCACTACCATGAACCTCCTGAGGCAATCCTATGAGGACTCCAGCAACCAAG	2735
Qy	4131	AAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTA	4190

Db	2736	 AAGAGGAGGGGCCAAGCACCTTCCCTGACCTGGAGTCCGAGTTCCAAGCAGCACTCAGTA	2795
Qy	4191	AGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCA	4250
Db	2796	 GGAAGGTGGCCGAGTTGGTTCATTTTCTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCA	2855
Qy	4251	CAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTGAGATCT	4310
Db	2856	 CAAAGGCAGAAATGCTGGGGAGTGTGTCGGAAATTGGCAGTATTTCTTTCTGTGATCT	2915
Qy	4311	TCGGCAAAGCCTCTGAGTCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACC	4370
Db	2916	 TCAGCAAAGCTTCCAGTTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACC	2975
Qy	4371	CCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGG	4430
Db	2976	 CCATCGGCCACTTGTACATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGG	3035
Qy	4431	GTGATAATCAGATCATGCCCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAA	4490
Db	3036	 GTGACAATCAGATCATGCCCCAAGGCAGGCCTCCTGATAATCGTCTTGCCATAATCGCAA	3095
Qy	4491	TGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGT	4550
Db	3096	 GAGAGGGCGACTGTGCCCTTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGT	3155
Qy	4551	ATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGG	4610
Db	3156	 TTGAGGGGAGGGAAGACAGTATCTTGGGGGATCCCAAGAAGCTGCTCACCCAACATTTCTG	3215
Qy	4611	TGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGT	4669
Db	3216	 TGCAGGAAAAC TACCTGGAGTACCGGCAGGTCCCCGGCAGTGATCCTGCATGTTATGAAT	3275
Qy	4670	TCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGA	4729
Db	3276	 TCCTGTGGGGTCCAAGGGCCCTCGTTGAAACCAGCTATGTGAAAGTCCTGCACCATATGG	3335
Qy	4730	TCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAG	4789
Db	3336	 TAAAGATCAGTGGAGGACCTCACATTTCTTACCCACCCCTGCATGAGTGGGTTTGTAGAG	3395
Qy	4790	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGC	4849
Db	3396	 AGGGGGAAGAGTGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGGGTCTGGGC	3455
Qy	4850	CAGTGCACCTTCCAGGGCCGCTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCCA	4909
Db	3456	 CAGTGCACCTTCCGGGGCCGCATCCCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCCCA	3515
Qy	4910	TTCTTCACTC--TGAAGAGAGCGGTGAGTGTCTCAGTAGTAGGTTTCTGTTCATTGGG	4967
Db	3516	 TTCTTCACTCTTTGAAGCGAGCAGTCAGCATCTTAGTAGTGGGTTTCTGTTCGTGTTGGA	3575
Qy	4968	TGACTTGGAGATTTATCTTTGTCTCTTTTGGAAATTGTTCAAATGTTTTTTTAAAGGGA	5027
Db	3576	 TGACTTTGAGATTATCTTTGTTTCTGTTGGAGTTGTTCAAATG-TTCCTTTTAACGGA	3634
Qy	5028	TGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTCACAC--AGTTCGTG	5085

```

Db      3635 TGGTTGAATGAGCGTCAGCATCCAGGTTTATGAATGACAGTAGTCACACATAGTGCTGTT 3694
Qy      5086 TATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTT 5145
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3695 TATATAGTTTAGGAGTAAGAGTCTTGTTTTTTACTCAAATTGGGAAATCCATTCCATTTT 3754
Qy      5146 GTGAATTGGG--ATAATAACAGCAGTGGAAATAAGTA----CTTAGAAATGTGA-AAAATG 5198
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3755 GTGAATTGTGACATAATAATAGCAGTGGTAAAAGTATTTGCTTAAAATTGTGAGCGAATT 3814
Qy      5199 AGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTT 5258
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3815 AGCAATAACATACATGAGAT----AACTCAAGAAATCAAAGATAGTTGATTCTTGCCCTT 3870
Qy      5259 ATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGCGCT 5318
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3871 GTACCTCAATCTATTCTGTAAAA---TTAAACAAATATGCAAACCAGGATTTCCCTTGACT 3927
Qy      5319 TCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCAGTGGCTCT 5378
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3928 TCTTTGAGAATGCAAGCGAAATTAAATCTGAATAAATAATTCTTCCTCTTCAGTGGCTCG 3987
Qy      5379 TTTCTTCTCCATGCACTGAGCATCTGCTTTTTTGGAGGCCCTGGGTTAGTAGTGGAGATG 5438
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3988 TTTCTTTTCCGTTCACTCAGCATCTGCTCTGTGGGAGGCCCTGGGTTAGTAGTGGGGATG 4047
Qy      5439 CTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCAC 5498
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4048 CTAAGGTAAGCCAGACTCACGCCTACCCATAGGGCTGTAGAGCCTAGGACCTGCAGTCAT 4107
Qy      5499 GTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGG 5558
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4108 ATAATTAAGGTGGTGAGAAAGTCTGTAAAGATGTAGAGGAAATGTAAGAGAGGGGTGAGGG 4167
Qy      5559 TGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCATGC 5595
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4168 TGTGGCGCTCCGGGTGAGAGTAGTGGAGTGTCAGTGC 4204

```

RESULT 7

US-11-323-964-28

; Sequence 28, Application US/11323964

; Publication No. US20060159689A1

; GENERAL INFORMATION:

; APPLICANT: Chiang, Chih-Sheng

; APPLICANT: Simard, John J.L.

; APPLICANT: Diamond, David C.

; APPLICANT: Bot, Adrian Ion

; APPLICANT: Liu, Xiping

; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED

; TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS

; FILE REFERENCE: MANNK.050CP1

; CURRENT APPLICATION NUMBER: US/11/323,964

; CURRENT FILING DATE: 2005-12-29

; PRIOR APPLICATION NUMBER: 11/155,288

; PRIOR FILING DATE: 2005-06-17

; PRIOR APPLICATION NUMBER: PCT/US2005/021836

; PRIOR FILING DATE: 2005-06-17

; PRIOR APPLICATION NUMBER: 60/580,969

; PRIOR FILING DATE: 2004-06-17

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 4204
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-323-964-28

Query Match 31.1%; Score 1762.6; DB 9; Length 4204;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 2315; Conservative 0; Mismatches 474; Indels 68; Gaps 20;

```
Qy      2790 AGGGACCCCCATCTGGTCTAAAGACAGAGCGGTCCCAGGATCTGCCATGCGTTCCGGGTGA 2849
      |||| |||| || |||| | ||| || ||||| ||||| ||||| |||||
Db      1365 AGGGGCCCTATGTGGTGGACAGATGCAGTGGTCCTAGGATCTGCCAAGCATCCAGGTGA 1424

Qy      2850 GGAACATGAGGGAGGACTGAGGGTACCCAGGACCAGAACTGA-GGGAGACTGCACAG 2908
      || ||||| ||||| ||||| ||||| || ||||| || ||||| |||||
Db      1425 AGAGACTGAGGGAGGATTGAGGGTACCCCTGGGACAGAATGCGGACTGGGGGCCCCATAA 1484

Qy      2909 AAATCAGCCCTGCCCCTGCTGTACCCCAGAGAGCATGGGCTGGGCCGTCTGCCGAGGTC 2968
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1485 AAATCTGCCCTGCTCCTGTCTTACCTCAGAGAGCCTGGGCAGGGCTGTCAGCTGAGGTC 1544

Qy      2969 CTTCCGTTATCCTGGGATCATTGATGTCAGGGACGGGGAGGCCTTGGTCTGAGAAGGCTG 3028
      | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1545 CCTCCATTATCCTAGGATCACTGATGTCAGGGAAGGGGAAGCCTTGGTCTGAGGGGGCTG 1604

Qy      3029 CGCTCAGGTCAGTAGAGGGAGCGTCCCAGGCCCTGCCAGGAGTCAAGGTGAGGACCAAGC 3088
      | ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
Db      1605 CACTCAGGGCAGTAGAGGGAGGCTCTCAGACCCTACTAGGAGTGGAGGTGAGGACCAAGC 1664

Qy      3089 GGGCACCTCACCCAGGACACATTAATTCCAATGAATTTTGATATCTCTTGCTG-CCCTTC 3147
      | | ||||| |||| | ||||| ||||| ||||| ||||| ||||| |||||
Db      1665 AGTCTCTCACCCAGGGTACATGGACTTCAATAAATTTGGACATCTCTCGTTGTCTTCTTC 1724

Qy      3148 CCCAAGGACCTAGGCACGTGTGGCCAGATGTTTGTCCCCTCCTGTCTTCCATTCCCTTAT 3207
      | ||||| || || || ||||| ||||| ||||| ||||| ||||| |||||
Db      1725 CGGGAGGACCTGGGAATGTATGGCCAGATGTGGGTCCCCTCATGTTTTTCTGTACCATAT 1784

Qy      3208 CATGGATGTGAACCTCTTG--ATTTGGATTTCTCAGACCAGCAAAAGGGCAGGATCCAGGC 3265
      || | ||||| |||| || | ||||| ||||| ||||| ||||| |||||
Db      1785 CAGGTATGTGAGTTC TTGACATGAGAGATTCTCAGGCCAGCAGAAGGGAGGGAT-TAGGC 1843

Qy      3266 CCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCCACTGCATGAG 3325
      ||| |||| ||| | ||||| ||||| ||||| ||||| ||||| |||||
Db      1844 CCTATAAGGAGAAAGGTGAGGGCCCTGAGTGAGCACAGAGGGGATCCTCCACCCCAGTAG 1903

Qy      3326 AGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGCCAGGGCTGTG 3385
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1904 AGTGGGGACCTCACAGAGTCTGGCCAACCCTCCTGACAGTTCTGGGAATCCGTGGCTGCG 1963

Qy      3386 CTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCTC-----CTGGAGCTCCAGGA 3438
      |||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db      1964 TTTGCTGTCTGCACATTGGGGGCGCGTGGATTCTCTCTCCAGGAATCAGGAGCTCCAGGA 2023

Qy      3439 ACCAGGCAGTGAGGCCTTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATGCAC 3498
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      2024 ACAAGGCAGTGAGGACTTGGTCTGAGGCAGTGTCTCAGGTCACAGAGTAGAGGGGGCTC 2083

Qy      3499 AGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCACAG 3558
      || ||||| | ||||| ||||| || || || ||||| ||||| ||||| |||||
```

Db 2084 AGATAGTGCCAACGGTGAAGGTTTGCCTTGGATTCAAACCAAGGGCCCCACCTGCCCCAG 2143

Qy 3559 GACACATAGGACTCCACAGAGTCTGGCCTCA-CCTCCCTACTGTCAGTCCTGTAGAATCG 3617
 ||||| ||||| || | ||||| |||| | ||| ||||| || ||

Db 2144 AACACAT-GGACTCCAGAGCGCTGGCCTCACCTCAATACTTTCAGTCCTGCAGCCTCA 2202

Qy 3618 ACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTTCAGGTTTTCAGG 3676
 | | ||||| ||||| || ||||| ||||| ||||| ||||| |||||

Db 2203 GCATGCGCTGGCCGGATGTACCCTGAGGTGCCCTCTCACTTCCTCCTTCAGGTTCTGAGG 2262

Qy 3677 GGACAGGCCAACCCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGAAG 3736
 ||||| ||| ||||| || ||| | | || | |||||

Db 2263 GGACAGGCTGACCTGGAGGACCAGAGGCCCGGAGGAGCACTG-----AAGGAGAAG 2315

Qy 3737 ATCTGTAAGTAGGCCTTTGTAGAGTCTCCAAGG-----TTCAGTTCTCAGCTGAGGCCT 3791
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2316 ATCTGTAAGTAAGCCTTTGTAGAGCCTCCAAGGTTCCATTCACTAGTCTCAGCTGAGGTCT 2375

Qy 3792 CTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACAC 3851
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2376 CTCACATGCTCCCTCTCTCCCCAGGCCAGTGGGTCTCCATTGCCCAGCTCCTGCCCACAC 2435

Qy 3852 TCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCA 3911
 ||| |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2436 TCCCGCCTGTTGCCCTGACCAGAGTCATCATGCCTCTTGAGCAGAGGAGTCAGCACTGCA 2495

Qy 3912 AGCCTGAGGAAGCCCTTGAGGCCCCAACAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCT- 3970
 ||||| |||| ||||| |||| | ||||| ||||| ||||| |||||

Db 2496 AGCCTGAAGAAGGCCCTTGAGGCCCCAGGAGAGGCCCTGGGCCTGGTGGGTGCGCAGGCTC 2555

Qy 3971 -----GCCACCTCCTCCTCCTCCTCCTGCTGGTCCCTGGGCACCTGG 4010
 || ||||| ||||| || ||||| || |||||

Db 2556 CTGCTACTGAGGAGCAGGAGGCTGCCTCCTCCTCTTCTACTCTAGTTGAAGTCACCCTGG 2615

Qy 4011 AGGAGGTGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCT 4070
 ||||| |||| | |||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2616 GGGAGGTGCCCTGCTGCCGAGTCACCAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCC 2675

Qy 4071 TTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTG 4130
 | ||||| |||| | |||| ||||| |||| |||| ||||| ||||| |||||

Db 2676 TCCCACTACCATGAATACCTCTCTGGAGCCAATCCTATGAGGACTCCAGCAACCAAG 2735

Qy 4131 AAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTA 4190
 ||||| ||||| ||||| | ||||| ||||| ||||| ||||| |||||

Db 2736 AAGAGGAGGGGCCAAGCACCTTCCCTGACCTGGAGTCCGAGTTCCAAGCAGCACTCAGTA 2795

Qy 4191 AGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCA 4250
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2796 GGAAGGTGGCCGAGTTGGTTCATTTTCTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCA 2855

Qy 4251 CAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCCTGAGATCT 4310
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2856 CAAAGGCAGAAATGCTGGGGAGTGTGCTCGGAAATTGGCAGTATTTCTTTCCTGTGATCT 2915

Qy 4311 TCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACC 4370
 || ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Db 2916 TCAGCAAAGCTTCCAGTTCCTTGCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACC 2975

Qy 4371 CCACCGGCCACTCCTATGTCCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGG 4430
 ||| ||||| || || |||| ||||| || ||||| ||||| |||||

Db 2976 CCATCGGCCACTTGTACATCTTTGCCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGG 3035

Qy	4431	GTGATAATCAGATCATGCCCCAAGACAGGCTTCCTGATAATGTCTCTGGTCATGATTGCAA	4490
Db	3036	GTGACAATCAGATCATGCCCCAAGGCAGGCTTCCTGATAATCGTCCTGGCCATAATCGCAA	3095
Qy	4491	TGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGT	4550
Db	3096	GAGAGGGCGACTGTGCCCCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGT	3155
Qy	4551	ATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGG	4610
Db	3156	TTGAGGGGAGGGAAGACAGTATCTTGGGGGATCCCAAGAAGCTGCTCACCCAACATTTTCG	3215
Qy	4611	TGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGT	4669
Db	3216	TGCAGGAAAAC TACCTGGAGTACCGGCAGGTCCCCGGCAGTGATCCTGCATGTTATGAAT	3275
Qy	4670	TCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCTTGAGTATGTGA	4729
Db	3276	TCCTGTGGGGTCCAAGGGCCCTCGTTGAAACCAGCTATGTGAAAGTCTGCACCATATGG	3335
Qy	4730	TCAAGGTCAGTGCAAGAGTTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAG	4789
Db	3336	TAAAGATCAGTGGAGGACCTCACATTTCTACCCACCCCTGCATGAGTGGGTTTGTAGAG	3395
Qy	4790	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGC	4849
Db	3396	AGGGGGAAGAGTGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGGGGTCTGGGC	3455
Qy	4850	CAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCA	4909
Db	3456	CAGTGCACCTTCCGGGGCCGCATCCCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCCA	3515
Qy	4910	TTCTTCACTC--TGAAGAGAGCGGTCAAGTCTCAGTAGTAGGTTTCTGTTCTATTGGG	4967
Db	3516	TTCTTCACTCCTTTGAAGCGAGCAGTCAGCATTCCTTAGTAGTGGGTTTCTGTTCTGTTGGA	3575
Qy	4968	TGACTTGGAGATTTATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTTAAGGGA	5027
Db	3576	TGACTTTGAGATTATTCTTTGTTTCTGTTGAGTTGTTCAAATG-TTCCTTTTAACGGA	3634
Qy	5028	TGGTTGAATGAACTTCAGCATCCAAGTTTATGAATGACAGCAGTCACAC--AGTTCGTG	5085
Db	3635	TGGTTGAATGAGCGTCAGCATCCAGGTTTATGAATGACAGTAGTCACACATAGTGCTGTT	3694
Qy	5086	TATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTT	5145
Db	3695	TATATAGTTTAGGAGTAAGAGTCTTGTTTTTTACTCAAATTGGGAAATCCATTCCATTTT	3754
Qy	5146	GTGAATTGGG--ATAATAACAGCAGTGGAATAAGTA----CTTAGAAATGTGA-AAAATG	5198
Db	3755	GTGAATTGTGACATAATAATAGCAGTGGTAAAAGTATTTGCTTAAAATTGTGAGCGAATT	3814
Qy	5199	AGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCCTT	5258
Db	3815	AGCAATAACATACATGAGAT----AACTCAAGAAATCAAAGATAGTTGATTCTTGCCCTT	3870
Qy	5259	ATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGCATACCTGGATTTCCTTGGCT	5318
Db	3871	GTACCTCAATCTATTCTGTAAAA---TTAAACAAATATGCAAACCAGGATTTCCTTGACT	3927

Qy	5319	TCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCAC	5378
Db	3928	TCTTTGAGAATGCAAGCGAAATTAAATCTGAATAAATAATTCTTCCTCTTCACTGGCTCG	3987
Qy	5379	TTTCTTCTCCATGCAC	5438
Db	3988	TTTCTTTTCCGTTCACTCAGCATCTGCTCTGTGGGAGGCCCTGGGTTAGTAGTGGGGATG	4047
Qy	5439	CTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCAC	5498
Db	4048	CTAAGGTAAGCCAGACTCACGCCTACCCATAGGGCTGTAGAGCCTAGGACCTGCAGTCAT	4107
Qy	5499	GTAATCGAGGTGGCAAGATGTCTCTAAAGATGTAGGGAAAAGTGAGAGAGGGGTGAGGG	5558
Db	4108	ATAATTAAGGTGGTGAGAAGTCTGTAAAGATGTAGAGGAAATGTAAGAGAGGGGTGAGGG	4167
Qy	5559	TGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTC	5595
Db	4168	TGTGGCGCTCCGGGTGAGAGTAGTGGAGTGTCAGTGC	4204

Db	539	ACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCACGCTTTTGCCTGCACTCT	598
Qy	3855	TGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGC	3914
Db	599	TGCCTGCTGCCCTGACCAGAGTCATCATGTCTTCTGAGCAGAAGAGTCAGCACTGCAAGC	658
Qy	3915	CTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCA	3974
Db	659	CTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGGTGGGTGCACAGGCTCCTA	718
Qy	3975	C-----CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGG	4011
Db	719	CTACTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTCTGGTCCCTGGCACCCTGG	778
Qy	4011	AGGAGGTGCCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCT	4070
Db	779	AGGAAGTGCCCTGCTGCTGAGTCAGCAGGTCTCCTCCCCAGAGTCCTCAGGGAGCCTCTGCCT	838
Qy	4071	TTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTG	4130
Db	839	TACCCACTACCATCAGCTTCACTTGCTGGAGGCAACCCAATGAGGGTTCCAGCAGCCAAG	898
Qy	4131	AAGAGGAGGGGCCAAGCACCTCTTGATCTCTGGAGTCCTTGTTCCGAGCAGTAATCACTA	4190
Db	899	AAGAGGAGGGGCCAAGCACCTCGCCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTA	958
Qy	4191	AGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCA	4250
Db	959	ACAAGGTGGATGAGTTGGCTCATTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCA	1018
Qy	4251	CAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACTGTTTTCTTGATATCT	4310
Db	1019	CAAAGGCAGAAATGCTGGAGAGAGTCATCAAAAATTACAAGCGCTGCTTTCTTGATATCT	1078
Qy	4311	TCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACC	4370
Db	1079	TCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACC	1138
Qy	4371	CCACCGGCCACTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGG	4430
Db	1139	CCGCCAGCAACACCTACACCTTGTCACCTGCCTGGGCCTTTCTATGATGGCCTGCTGG	1198
Qy	4431	GTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAA	4490
Db	1199	GTAATAATCAGATCTTTCCCAAGACAGGCTTCTGATAATCGTCCTGGGCACAATTGCAA	1258
Qy	4491	TGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGT	4550
Db	1259	TGGAGGGCGACAGCGCCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGT	1318
Qy	4551	ATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGG	4610
Db	1319	ATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGG	1378
Qy	4611	TGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGT	4669
Db	1379	TGCAGGAAAAGTACCTGGAGTACCGGCAGGTACCGGCAGTAATCCTGCGCGCTATGAGT	1438
Qy	4670	TCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGA	4729
Db	1439	TCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGGAGCATGTGG	1498

Qy	4730	TCAAGGTCAGTGCAGAGTTTCGTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAG	4789
Db	1499	TCAGGGTCAATGCAAGAGTTCGCATTGCCATCCCATCCCTGCGTGAAGCAGCTTTGTTAG	1558
Qy	4790	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG-----GGACT	4845
Db	1559	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAGGGCTGTGGGGAAGGGGCAGGGCT	1618
Qy	4846	GGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGG	4905
Db	1619	GGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCTTGCCTCGTGTAAACATGAGG	1676
Qy	4906	CCCATTCTTCACTC-----TGAAGAGAGCGGTCAAGTGTCTCAGTAGTAGTTTCTGTCT	4961
Db	1677	CCCATTCTTCACTCTGTTTGAAGAAAATAGTCAAGTGTCTTAGTAGTGGGTTTCTATTTT	1736
Qy	4962	ATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAAATTGTTCAAATGTTTTTTTTT	5021
Db	1737	GTTGGATGACTTGGAGATTTATCTCTGTTTCCCTTTTACAATTGTTGAAATG-TTCCTTTT	1795
Qy	5022	AAGGGATGGTTGAATGAACCTTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTC	5081
Db	1796	AATGGATGGTTGAATTAACCTTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGC	1855
Qy	5082	TGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGAAATCCATTCTA	5141
Db	1856	TGTTAATATAGTTTAGGAGTAAGAGTCTTGTTTTTTATTTCAGATTGGGAAATCCGTTCTA	1915
Qy	5142	TTTTGTGAATTGGG---ATAATAACAGCAGTGAATAAGTACTTAGAAATGTGAAAAATG	5198
Db	1916	TTTTGTGAATTGGGACATAATAACAGCAGTGGAGTAAGTATTTAGAAGTGTG---AATT	1972
Qy	5199	AGCAGTAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTT	5258
Db	1973	CACCGTGAAATAGGTGAGAT-----AAATTAAAAGATACTTAATTCCCGCCTT	2020
Qy	5259	ATACCTCAGTCTATTCTGTAAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCT	5318
Db	2021	ATGCCCTCAGTCTATTCTGTAAAAATTTAAAAATATATATGCATACCTGGATTTCCTTGGCT	2080
Qy	5319	TCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCT	5378
Db	2081	TC---GTGAATGTAAGAGAAATTAAATCTGAATAAATAATTCTTTCTGTAACTGGCTCA	2137
Qy	5379	TTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAAGGCCCTGGGTTAGTAGTGGAGATG	5438
Db	2138	TTTCTTCTCTATGCACTGAGCATCTGCTCTGTGGAAGGCCCAGGATTAGTAGTGGAGATA	2197
Qy	5439	CTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCAC	5498
Db	2198	CTAGGGTAAGCCAGACACACACCTACCGATAGGGTATTAAGAGTCTAGGAGCGCGGTCAT	2257
Qy	5499	GTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGGAAAAGTGAGAGAGGGGTGAGGG	5558
Db	2258	ATAATTAAGGTGACAAGATGTCCTCTAAGATGTAGGGGAAAAGT----AACGAGTGTGGG	2313
Qy	5559	TGTGGGGCTCCGGGTGAGAGTGGTGGAGTGTCAATGCCCTGAGCTGGGGCATTGTGGGCT	5618
Db	2314	TATGGGGCTCCAGGTGAGAGTGGTGGGTGTAATTCCTGTG-TGGGGCTTTTGGGCT	2372

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-11-253-240-14

Query Match 29.6%; Score 1678.8; DB 8; Length 2531;
Best Local Similarity 84.4%; Pred. No. 0;
Matches 2074; Conservative 0; Mismatches 317; Indels 65; Gaps 14;

```
Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
          |||||
Db       1  GGATCCAGGCCCTGCCTGGAGAAATGTGAGGGCCCTGAGTGAACACAGTGGGGATCATCC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTCACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
          |||
Db      61  ACTCCATGAGAGTGGGGACCTCACAGAGTCCAGCCTACCCTCTTGATGGCACTGAGGGAC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435
          |
Db     121  CGGGGCTGTGCTTACAGTCTGCACCCTAAGGGCCCATGGATTCTCTCCTAGGAGCTCCA 180

Qy      3436 GGAACCAGGCAGTGAGGCCCTGGTCTGAGACAGTATCCTCAGGTCACAGAGCAGAGGATG 3495
          |||||
Db     181  GGAACAAGGCAGTGAGGCCCTGGTCTGAGACAGTGTCTCAGGTTACAGAGCAGAGGATG 240

Qy      3496 CACAGGGTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 3555
          |||||
Db     241  CACAGGCTGTGCCAGCAGTGAATGTTTGCCCTGAATGCACACCAAGGGCCCCACCTGCCA 300

Qy      3556 CAGGACACATAGGACTCCACAGAGTCTGGCCTCACCTCCCTACTGTCAGTCTGTAGAAT 3615
          ||
Db     301  CAAGACACATAGGACTCCAAAGAGTCTGGCCTCACCTCCCTACCATCAATCCTGCAGAAT 360

Qy      3616 CGACCTCTGCTGGCCGGCTGTACCCTGA-GTACCCTCTCACTTCCTCCTTCAGGTTTTCA 3674
          |||||
Db     361  CGACCTCTGCTGGCCGGCTATACCCTGAGGTGCTCTCTCACTTCCTCCTTCAGGTTCTGA 420

Qy      3675 GGGGACAGGCCAACCAGAGGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGA 3734
          |
Db     421  GCAGACAGGCCAACC--GGAGACAGGATTCCCTGGAGGCCACAGAGGAGCACCAAGGAGA 478

Qy      3735 AGATCTGTAAGTAGGCCTTTGTGTAGAGTCTCCAAGGTTCA GTTCTCAGCTGAGGCCTCTC 3794
          |||||
Db     479  AGATCTGTAAGTAAGCCTTTGTGTAGAGCCTCTAAGATTG GTTCTCAGCTGAGGTCTCTC 538

Qy      3795 ACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCCCAGCTCCTGCCACACTCC 3854
          |||
Db     539  ACATGCTCCCTCTCTCCGTAGGCCTGTGGGTCCCCATTGCCCAGCTTTTGCTGCACTCT 598

Qy      3855 TGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGC 3914
          |||||
Db     599  TGCCTGCTGCCCTGAGCAGAGTCATCATGTCTCTTGAGCAGAAGAGTCAGCACTGCAAGC 658

Qy      3915 CTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCA 3974
          |||||
Db     659  CTGAGGAAGGCGTTGAGGCCCAAGAAGAGGCCCTGGGCCTGGTGGGTGCGCAGGCTCCTA 718

Qy      3975 C-----CTCCTCCTCCTCTCCTCTGGTCCTGGGCACCCTGG 4010
          |
Db     719  CTA CTGAGGAGCAGGAGGCTGCTGTCTCCTCCTCCTCTCCTCTGGTCCCTGGCACCCTGG 778

Qy      4011 AGGAGGTGCCCAGTGTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCT 4070
          |||||
```

Db	779	AGGAAGTGCCTGCTGCTGAGTCAGCAGGTCCTCCCCAGAGTCCTCAGGGAGCCTCTGCCT	838
Qy	4071	TTCCCACTACCATCAACTTCACCTCGACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTG	4130
Db	839	TACCCACTACCATCAGCTTCACCTGCTGGAGGCAACCCAATGAGGGTTCAGCAGCCAAG	898
Qy	4131	AAGAGGAGGGGCCAAGCACCTCTTGATCCTGGAGTCCTTGTTCCGAGCAGTAATCACTA	4190
Db	899	AAGAGGAGGGGCCAAGCACCTCGCTGACGCAGAGTCCTTGTTCCGAGAAGCACTCAGTA	958
Qy	4191	AGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCA	4250
Db	959	ACAAGGTGGATGAGTTGGCTCATTTTTCTGCTCCGCAAGTATCGAGCCAAGGAGCTGGTCA	1018
Qy	4251	CAAAGGCAGAAATGCTGGAGAGTGTCAATCAAAAATTACAAGCACTGTTTTCTGAGATCT	4310
Db	1019	CAAAGGCAGAAATGCTGGAGAGAGTCAATCAAAAATTACAAGCGCTGCTTTCTGTGATCT	1078
Qy	4311	TCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACC	4370
Db	1079	TCGGCAAAGCCTCCGAGTCCCTGAAGATGATCTTTGGCATTGACGTGAAGGAAGTGGACC	1138
Qy	4371	CCACCGGCCACTCCTATGTCTTGTCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGG	4430
Db	1139	CCACCGAACACCTACACCTTGTCACCTGCCTGGGCCTTTCTATGATGGCCTGCTGG	1198
Qy	4431	GTGATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCTGGTCATGATTGCAA	4490
Db	1199	GTAATAATCAGATCTTTCCCAAGACAGGCTTCTGATAATCGTCTGGGCACAATTGCAA	1258
Qy	4491	TGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGT	4550
Db	1259	TGGAGGGCGACAGCGCTCTGAGGAGGAAATCTGGGAGGAGCTGGGTGTGATGGGGGTGT	1318
Qy	4551	ATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTTGG	4610
Db	1319	ATGATGGGAGGGAGCACACTGTCTATGGGGAGCCCAGGAACTGCTCACCCAAGATTGGG	1378
Qy	4611	TGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGT	4669
Db	1379	TGCAGGAAAAGTACCTGGAGTACCGGCAGGTACCCGGCAGTAATCCTGCGCGCTATGAGT	1438
Qy	4670	TCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGA	4729
Db	1439	TCCTGTGGGGTCCAAGGGCTCTGGCTGAAACCAGCTATGTGAAAGTCCTGAGCATGTGG	1498
Qy	4730	TCAAGGTCAGTGCAAGAGTTTCGCTTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAG	4789
Db	1499	TCAGGTCATGCAAGAGTTTCGCTTACCCATCCCTGCGTGAAGCAGCTTTGTTAG	1558
Qy	4790	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGG---GGACT	4845
Db	1559	AGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGGCTGTGGGGAGGGGCAGGGCT	1618
Qy	4846	GGGCCAGTGCACCTTCCAGGGCCGCTCCAGCAGCTTCCCCTGCCTCGTGTGACATGAGG	4905
Db	1619	GGGCCAGTGCATCTAACA--GCCCTGTGCAGCAGCTTCCCCTGCCTCGTGTAAACATGAGG	1676
Qy	4906	CCCATTCCTTCACTC---TGAAGAGAGCGGTGAGTGTTCAGTAGTAGGTTCTGTTCT	4961
Db	1677	CCCATTCCTTCACTCTGTTTGAAGAAAAATAGTCAGTGTTCCTTAGTAGTGGGTTCTATTTT	1730

Qy	4962	ATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAAATGTTCAAATGTTTTTTTTT	5021
Db	1737		
Qy	5022	GTTGGATGACTTGGAGATTTATCTCTGTTTCCTTTTACAATTGTTGAAATG-TTCCTTTT	1795
Qy	5022	AAGGGATGGTTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACACAGTTC	5081
Db	1796		
Qy	5082	AATGGATGGTTGAATTAAC TTCAGCATCCAAGTTTATGAATCGTAGTTAACGTATATTGC	1855
Qy	5082	TGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATT CAGATTGGGAAATCCATTCTA	5141
Db	1856		
Qy	5142	TGTTAATATAGTTTAGGAGTAAGAGTCTTGT TTTTATT CAGATTGGGAAATCCGTTCTA	1915
Qy	5142	TTTTGTGAATTGGG---ATAATAACAGCAGTGGGAATAAGTACTTAGAAAATGTGAAAAATG	5198
Db	1916		
Qy	5199	TTTTGTGAATTGGGACATAATAACAGCAGTGGAGTAAGTATTTAG AAGTGTG---AATT	1972
Qy	5199	AGCAGTAAAATAGATGAGATAAAGAAC TAAAGAAATTAAGAGATAGTCAATCTTGCCTT	5258
Db	1973		
Qy	5259	CACCGTGAAATAGGTGAGAT-----AAATTAAGATACTTAATCCCGCCTT	2020
Qy	5259	ATACCTCAGTCTATTCTGTAAAATTTTAAAGATATATGCATACCTGGATTTCCTTGGCT	5318
Db	2021		
Qy	5319	ATGCCTCAGTCTATTCTGTAAAATTTAAAAATATATATGCATACCTGGATTTCCTTGGCT	2080
Qy	5319	TCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCTGTTCAGTGGCTCT	5378
Db	2081		
Qy	5379	TC---GTGAATGTAAGAGAAATTAAATCTGAATAAATAATTCTTTCTGTTAAGTGGCTCA	2137
Qy	5379	TTTCTTCTCCATGCAGTCTGAGCATCTGCTTTTTTGG AAGGCCCTGGGTTAGTAGTGGAGATG	5438
Db	2138		
Qy	5439	TTTCTTCTCTATGCAGTCTGAGCATCTGCTCTGTGGAAGGCC CAGGATTAGTAGTGGAGATA	2197
Qy	5439	CTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCAC	5498
Db	2198		
Qy	5499	CTAGGGTAAGCCAGACACACCTACCGATAGGGTATTAAGAGTCTAGGAGCGCGGTCAT	2257
Qy	5499	GTAATCGAGGTGGCAAGATGTCCTCTAAAGATGTAGGGGAAAAGT GAGAGAGGGGTGAGGG	5558
Db	2258		
Qy	5559	ATAATTAAGGTGACAAGATGTCCTCTAAGATGTAGGGGAAAAGT----AACGAGTGTGGG	2313
Qy	5559	TGTGGGGCTCCGGGTGAGAGTGGTGGAGTGCAATGCCCTGAGCTGGGGCATTTTGGGCT	5618
Db	2314		
Qy	5619	TATGGGGCTCCAGGTGAGAGTGGTCGGGTGTAAATTCCTGTG-TGGGGCCTTTTGGGCT	2372
Qy	5619	TTGGGAAACTGCAGTTTCCTTCTGGGGGAGCTGATTGTAATGATCTTGGGTGGATCC	5674
Db	2373		
Qy	5674	TTGGGAAACTCCATTTTCTTCTGAGGGATCTGATTCTAATGAAGCTTGGTGGGTCC	2428

```

;      ADDRESSEE: Felfe & Lynch
;      STREET: 805 Third Avenue
;      CITY: New York City
;      STATE: New York
;      ZIP: 10022
;
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
;      COMPUTER: IBM
;      OPERATING SYSTEM: PC-DOS
;      SOFTWARE: Wordperfect
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/11/253,240
;      FILING DATE: 17-Oct-2005
;      CLASSIFICATION:
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: US/09/579,543
;      FILING DATE: 26-May-2000
;      APPLICATION NUMBER: 09/583,850
;      FILING DATE:
;      APPLICATION NUMBER: PCT/US92/04354
;      FILING DATE: 22-MAY-1992
;      APPLICATION NUMBER: 07/807,043
;      FILING DATE: 12-DECEMBER-1991
;      APPLICATION NUMBER: 07/764,365
;      FILING DATE: 23-SEPTEMBER-1991
;      APPLICATION NUMBER: 07/728,838
;      FILING DATE: 9-JULY-1991
;      APPLICATION NUMBER: 07/705,702
;      FILING DATE: 23-MAY-1991
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Hanson, Norman D.
;      REGISTRATION NUMBER: 30,946
;      REFERENCE/DOCKET NUMBER: LUD 5353
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 688-9200
;      TELEFAX: (212) 838-3884
;
;      INFORMATION FOR SEQ ID NO: 17:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 2305 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;      MOLECULE TYPE: genomic DNA
;      FEATURE:
;      NAME/KEY: MAGE-51 gene
;      SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-11-253-240-17

```

```

Query Match          26.5%;  Score 1504.6;  DB 8;  Length 2305;
Best Local Similarity 83.7%;  Pred. No. 0;
Matches 1942;  Conservative 0;  Mismatches 304;  Indels 75;  Gaps 18;

```

```

Qy      3256 GGATCCAGGCCCTGCCAGGAAAAATATAAGGGCCCTGCGTGAGAACAGAGGGGGTCATCC 3315
         ||||| ||||| ||| | ||||| ||||| ||||| ||| |
Db      1 GGATCCAGGCCTTGCCAGGAGAAAGGTGAGGGCCCTGTGTGAGCACAGAGGGGACCATTC 60

Qy      3316 ACTGCATGAGAGTGGGGATGTACACAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC 3375
         || || || |||| || ||||| ||||| ||||| ||||| ||| |
Db      61 ACCCCAAGAGGGTGGAGACCTCACAGATTCCAGCCTACCCTCCTGTTAGCACTGGGGGCC 120

Qy      3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA 3435

```

[illegible]

Db	1020	TCAAGGAGCCGGTCACAAAGGCAGAAATGCTGGAGAGCGTCATCAAAAATTACAAGCGCT	1079
Qy	4296	GTTTTCTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACG	4355
Db	1080	GCTTTCTCTGAGATCTTCGGCAAAGCCTCCGAGTCCTTGACGCTGGTCTTTGGCATTGACG	1139
Qy	4356	TGAAGGAAGCAGACCCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCT	4415
Db	1140	TGAAGGAAGCGGACCCCCACAGCAACACCTACACCCTTGTCACCTGCCTGGGACTC--CT	1197
Qy	4416	ATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCC	4475
Db	1198	ATGATGGCCTGGTGGTT--TAATCAGATCATGCCCAAGACGGGCCTCTGATAATCGTCT	1255
Qy	4476	TGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGA	4535
Db	1256	TGGGCATGATTGCAATGGAGGGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGAGCTGG	1315
Qy	4536	GTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGC	4595
Db	1316	GTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGTCTGTGGGGAGCCCAGGAAGCTGC	1375
Qy	4596	TCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACGGCAGGTGCCGGACAGTGATCC	4655
Db	1376	TCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTACCGCAGGTGCCAGCAGTGATCC	1435
Qy	4656	CGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGT	4715
Db	1436	CATATGCTATGAGTTACTGTGGGGTCCAAGGGCACTCGCTGC-----TTGAAAGT	1485
Qy	4716	CCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTGA	4775
Db	1486	ACTGGAGCACGTGGTCAGGGTCAATGCAAGAGTTCCTCATTTCCCTACCCATCCCTGCATGA	1545
Qy	4776	AGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGG	4835
Db	1546	AGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGCTGCAGCCAGGGCCACTGC	1605
Qy	4836	GAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCC-TCGT	4894
Db	1606	GAGGGGGGCTGGGCCAGTGCACCTTCCAGGGCTCCGTCCAGTAGTTTCCCCTGCTTAAT	1665
Qy	4895	GTGACATGAGGCCCATTCTTCACTC--TGAAGAGAGCGGTGAGTGTCTCAGTAGTAGGT	4952
Db	1666	GTGACATGAGGCCCATTCTTCTCTCTTTGAAGAGAGCAGTCAACATTCTTAGTAGTGGGT	1725
Qy	4953	TTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAAATTGTTCAAATG	5012
Db	1726	TTCTGTTCTATTGGATGACTTTGAGATTTGTCTTTGTTCTCTTTTGGAAATTGTTCAAATG	1785
Qy	5013	TTTTTTTTTAAGGGATGGTTGAATGAACCTCAGCATCCAAGTTTATGAATGACAGCAGTC	5072
Db	1786	-TTCTTTTAATGGGTGGTTGAATGAACCTCAGCATTCAAATTTATGAATGACAGTAGTC	1844
Qy	5073	ACAC--AGTTCGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGA	5130
Db	1845	ACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCTTGTTTTTATTTCAGATTGGGA	1904
Qy	5131	AATCCATTCTATTTTGTGAATTGGG--ATAATAACAGCAGTGGAATAAGTACTTA-GAAA	5187
Db	1905	AATCCATTCCATTTTGTGAATTGGGACATAGTTACAGCAGTGGAATAAGTATTTCATTTAG	1964

Qy	5188	TGTGAAAAATGAGCAGTAAATAGATGAGATAAAGAAGCTAAAGAAATTAAGAGATAGTCA	5247
Db	1965	AAATGTGAATGAGCAGTAAACTGATGAGA-----TAAAGAAATTAAGAGATATTTA	2016
Qy	5248	ATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAA--TTTTTAAAGATATATGCATACCTG	5305
Db	2017	ATTCTTGCCCTTATA-CTCAGTCTATTCCGTAAAAATTTTTTTTTTAAAAATGTGCATACCTG	2075
Qy	5306	GATTTCCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAGAATTCTTCCT	5365
Db	2076	GATTTCCCTTGGCTTCTTTGAGAATGTAAGACAAATTAATCTGAATAAATCATTCTCCCT	2135
Qy	5366	GTTCACTGGCTCTTTTCTTCTCCATGCACTGAGCATCTGCTTTTTGGAAGGCCCTGGGTT	5425
Db	2136	GTTCACTGGCTCATTTATTCTCTATGCACTGAGCATTTGCTCTGTGGAAGGCCCTGGGTT	2195
Qy	5426	AGTAGTGAGATGCTAAGGTAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAG	5485
Db	2196	AATAGTGAGATGCTAAGGTAAGCCAGACTCACCCCTACCCACAGGGTAGTAAAGTCTAG	2255
Qy	5486	GAGCTGCAGTCACGTAATCGAGGTGGCAAGATGTCTCTTAA	5526
Db	2256	GAGCAGCAGTCATATAATTAAGGTGGAGAGATGCCCTCTAA	2296

US-11-253-240-16

; Sequence 16, Application US/11253240

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;
 ; van der Bruggen, Pierre; Boon-Falleur, Thierry

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

```
; NUMBER OF SEQUENCES: 30
```

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York City

STATE: New York

; ZIP: 10022

; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
```

```
;          COMPUTER:  IBM
```

```
;      OPERATING SYSTEM: PC-DOS
```

```
; SOFTWARE: Wordperfect
```

```
;      CURRENT APPLICATION DATA:
```

; APPLICATION NUMBER: US/11/253,240

; FILING DATE: 17-Oct-2005

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/579,543

; FILING DATE: 26-May-2000

; APPLICATION NUMBER: 09/583,850

; FILING DATE:

; APPLICATION NUMBER: PCT/US92/04354

; FILING DATE: 22-MAY-1992

; APPLICATION NUMBER: 07/807,043

; FILING DATE: 12-DECEMBER-1991

```

; FILING DATE: 23-SEPTEMBER-1991
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2226 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: MAGE-5 gene
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-253-240-16

```

Qy		3256 GGATCCAGGCCCTTGCCAGGAAAAAATAAAGGGCCCTGCGTGAACAGAGGGGGTCATCC	3315
Db	1	GGATCCAGGCCTTGCCAGGAGAAGGTGAGGGCCCTGTGTGAGCACAGAGGGGACCATTC	60
Qy		3316 ACTGCATGAGAGTGGGGATGTCA CAGAGTCCAGCCCACCCTCCTGGTAGCACTGAGAAGC	3375
Db	61	ACCCAAGAGGGGTGGAGACCTCACAGATTCCAGCCTACCCTCCTGTTAGCACTGGGGGCC	120
Qy		3376 CAGGGCTGTGCTTGCGGTCTGCACCCTGAGGGCCCGTGGATTCTCTTCCTGGAGCTCCA	3435
Db	121	TGAGGCTGTGCTTGCA GTCTGCACCCTGAGGGCCCATGCATTCTCTTCCAGGAGCTCCA	180
Qy		3436 GGAACCAGGCAGTGAGGCCCTTGGTCTGAGACAGTATCTCAGGTCACAGAGCAGAGGATG	3495
Db	181	GGAACAGACACTGAGGCCCTTGGTCTGAGGCCGTGCCCTCAGGTCACAGAGCAGAGGAGA	240
Qy		3496 CACAG----GGTGTGCCAGCAGTGAATGTTGCCCTGAATGCACACAAGGGCCCCACCT	3551
Db	241	TGCAGACGTCTAGTGCCAGCAGTGAACGTTTG CCTTGAATGCACATAATGGCCCCCATC	300
Qy		3552 GCCACAGGACACATAGGACTCCACAGAGTCTGGCCTCA-CCTCCCTACTGTGTCAGTCTGT	3610
Db	301	GCCCCAGAACATATGGGACTCCAGAGCACCTGGCCTCACCTCTCTACTGTGTCAGTCTGTC	360
Qy		3611 AGAATCGACCTCTGCTGGCCGGCTGTACCCTGAGTACCCTCTCACTTCCTCCTTCAGGTT	3670
Db	361	AGAATCAGCCTCTGCTTGCTTG TGTACCCTGAGGTGCCCTCTCACTTTTTCCTTCAGGTT	420
Qy		3671 TTCAGGGGACAGGCCAACCCAGAGGAC-----AGGATTCCCTGGAGGCCACA	3717
Db	421	CTCAGGGGACAGGCTGACCAGGATCACCAGGAAGCTCCAGAGGATCCCAGGAGGCCCTA	480
Qy		3718 GAGGAGCACC-AAGGAGAAGATCTGTAAGTAGGCCTTTGTTAGAGTCTCCAAGGTT CAGT	3776

Db	481	GAGGAGCACCAAAGGAGAAGATCTGTAAGTAAGCCTTTGTTAGAGCCTCCAAGGTTTCAGT	540
Qy	3777	TCTCAGCTGAGGCCTCTCACACACTCCCTCTCTCCCCAGGCCTGTGGGTCTTCATTGCC	3836
Db	541	TTTTAGCTGAGGCTTCTCACATGCTCCCTCTCTCTCCAGGCCAGTGGGTCTCCATTGCC	600
Qy	3837	AGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAGTCATCATGTCTCTTGAGCAGA	3896
Db	601	AGCTCCTGCCCACACTCCTGCCTGTTGCGGTGACCAGAGTCGTTCATGTCTCTTGAGCAGA	660
Qy	3897	GGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCCAACAAGAGGCCCTGGGCCTGG	3956
Db	661	AGAGTCAGCACTGCAAGCCTGAGGAA-----	686
Qy	3957	TGTGTGTGCAGGCTGCCACCTCCTCCTCTCTCTGGTCTGGGCACCCTGGAGGAGG	4016
Db	687	-----CTCCTCTGGTCCCAGGCACCCTGGGGGAGG	716
Qy	4017	TGCCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCA	4076
Db	717	TGCCTGCTGCTGGGTCAACAGGTCTCTCAAGAGTCCTCAGGGAGCCTCCGCCATCCCA	776
Qy	4077	CTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGGGTTCAGCAGCCGTGAAGAGG	4136
Db	777	CTGCCATCGATTTCACCTCTATGGAGGCAATCCATTAAGGGCTCCAGCAACCAAGAAGAGG	836
Qy	4137	AGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGG	4196
Db	837	AGGGGCCAAGCACCTCCCCTGACCCAGAGTCTGTGTTCCGAGCAGCACTCAGTAAGAAGG	896
Qy	4197	TGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGG	4256
Db	897	TGGCTGACTTGATTTCATTTTCTGCTCCTCAAGTATTAAGTCAAGGAGCTGGTCACAAAGG	956
Qy	4257	CAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACTGTTTTCTGAGATCTTCGGCA	4316
Db	957	CAGAAATGCTGGAGAGCGTCATCAAAAATTACAAGCGCTGCTTTCCTGAGATCTTCGGCA	1016
Qy	4317	AAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCG	4376
Db	1017	AAGCCTCCGAGTCCTTGCAGCTGGTCTTTGGCATTGACGTGAAGGAAGCGGACCCACCA	1076
Qy	4377	GCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTG---	4433
Db	1077	GCAACACCTACACCTTGTACCTGCCTGGG--ACTCCTATGATGGCCTGCTGGTTGATA	1134
Qy	4434	ATAATCAGATCATGCCCAAGACAGGCTTCTGATAATTGTCTGGTCATGATTGCAATGG	4493
Db	1135	ATAATCAGATCATGCCCAAGACGGCCTCTGATAATCGTCTTGGGCATGATTGCAATGG	1194
Qy	4494	AGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATG	4553
Db	1195	AGGGCAAATGCGTCCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATG	1254
Qy	4554	ATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGTTGTC	4613
Db	1255	TTGGGAGGGAGCACAGTGTCTGTGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGTTGTC	1314
Qy	4614	AGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCC	4672

Db	1315	AGGAAAAC TACCTGGAGTACCGGCAGGTGCCCAGCAGTGCATCCCATATGCTATGAGTTAC	1374
Qy	4673	TGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAGTCCTTGAGTATGTGATCA	4732
Db	1375	TGTGGGGTCCAAGGGCACTCGCTG-----CTTGAAAGTACTGGAGCACGTGGTCA	1424
Qy	4733	AGGTCAGTGCAAGAGTTCGCTTTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGG	4792
Db	1425	GGGTCAATGCAAGAGTTCTCATTTCTACCCATCCCTGCGTGAAGCAGCTTTGAGAGAGG	1484
Qy	4793	AGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTGGGAGGGGGACTGGGCCAG	4851
Db	1485	AGGAAGAGGGAGTCTGAGCATGAGCTGCAGCCAGGGCCACTGCGAGGGGGGCTGGGCCAG	1544
Qy	4853	TGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCC-TCGTGTGACATGAGGCCCAT	4911
Db	1545	TGCACCTTCCAGGGCTCCGTCCAGTAGTTTCCCTGCCTTAATGTGACATGAGGCCCAT	1604
Qy	4912	CTTCACTC--TGAAGAGAGCGGTCAAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTG	4969
Db	1605	CTTCTCTCTTTGAAGAGAGCAGTCAACATTCTTAGTAGTGGGTTTCTGTTCTATTGGATG	1664
Qy	4970	ACTTGGAGATTATCTTTGTTCTCTTTTGAATTGTTCAAATGTTTTTTTTTAAGGGATG	5029
Db	1665	ACTTTGAGATTGTCTTTGTTTCTTTTGAATTGTTCAAATGTTTC-TTTAATGGGTG	1723
Qy	5030	GTTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTCACAC--AGTCTGTGTA	5087
Db	1724	GTTGAATGAAC TTCAGCATTCAAATTTATGAATGACAGTAGTCACACATAGTGCTGTTTA	1783
Qy	5088	TATAGTTTAAGGGTAAGAGTCTTGTTTATTCAGATTGGGAAATCCATTCTATTTTGT	5147
Db	1784	TATAGTTTAGGAGTAAGAGTCTTGTTTTTATTCAGATTGGGAAATCCATTCCATTTTGT	1843
Qy	5148	GAATTGGG--ATAATAACAGCAGTGGAAATAAGTACTTA-GAAATGTGAAAAATGAGCAGT	5204
Db	1844	GAATTGGGACATAGTTACAGCAGTGGAAATAAGTATTCATTTAGAAATGTGAATGAGCAGT	1903
Qy	5205	AAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAGTCAATTCTTGCCTTATACCT	5264
Db	1904	AAAAC TGATGACA-----TAAAGAAAT TAAAAGATATTTAATTCTTGCTTATACTCA	1955
Qy	5265	CAGTCTATTCTGTAAAATTTTTTAAAGATATATGCATACCTGGATTTCCTTGGCCTCTTTG	5324
Db	1956	GTC TATTTCGGTAAAATTTTTTTTTTAAAAAATGTGCATACCTGGATTTCCTTGGCCTCTTTG	2015
Qy	5325	AGAATGTAAGAGAAATTAAATCTGAATAAAGAATTCTTCCTGTTCACTGGCTCTTTTCTT	5384
Db	2016	AGAATGTAAGACAAATTAAATCTGAATAAATCATTCTCCCTGTTCACTGGCTCATTAT	2075
Qy	5385	CTCCATGCACTGAGCATCTGCTTTTTTGAAGGCCCTGGGTTAGTAGTGAGATGCTAAGG	5444
Db	2076	CTCTATGCACTGAGCATTGCTCTGTGGAAGGCCCTGGGTTAATAGTGAGATGCTAAGG	2135
Qy	5445	TAAGCCAGACTCATACCCACCCATAGGGTCGTAGAGTCTAGGAGCTGCAGTCACGTAATC	5504
Db	2136	TAAGCCAGACTCACCCCTACCCACAGGGTAGTAAAGTCTAGGAGCAGCAGTCATATAATT	2195
Qy	5505	GAGGTGGCAAGATGTCTCTTAA	5526
Db	2196	AAGGTGGAGAGATGCCCTCTAA	2217

RESULT 12
 US-11-266-748A-87851
 ; Sequence 87851, Application US/11266748A
 ; Publication No. US20060134663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick
 ; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and
 ; TITLE OF INVENTION: Methods of Using the Same
 ; FILE REFERENCE: 55815-0102 (319189)
 ; CURRENT APPLICATION NUMBER: US/11/266,748A
 ; CURRENT FILING DATE: 2005-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105479.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105482.6
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105483.4
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105507.0
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105485.9
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105484.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: US 60/662,276
 ; PRIOR FILING DATE: 2005-03-14
 ; PRIOR APPLICATION NUMBER: US 60/700,293
 ; PRIOR FILING DATE: 2005-07-18
 ; NUMBER OF SEQ ID NOS: 483996
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 87851
 ; LENGTH: 1577
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-11-266-748A-87851

Query Match 20.9%; Score 1188.2; DB 8; Length 1577;
 Best Local Similarity 89.4%; Pred. No. 4.1e-299;
 Matches 1390; Conservative 0; Mismatches 133; Indels 32; Gaps 9;

Qy	3816	GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG	3875
Db	40	GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGTTGCCCTGACGAGAG	99
Qy	3876	TCATCATGTCTCTTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC	3935
Db	100	TCATCATGTCTCTTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC	159
Qy	3936	AACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCTCTCTCTGG	3995
Db	160	AACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCTCTCTCTGG	219
Qy	3996	TCCTGGGCACCTGGAGGAGGTGCCCCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC	4055
Db	220	TCCTGGGCACCTGGAGGAGGTGCCCCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC	279
Qy	4056	AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGG	4115

Db	280	AGGGAGCCTCCGCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGG	339
Qy	4116	GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTC	4175
Db	340	GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTC	399
Qy	4176	GAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATATCGAG	4235
Db	400	GAGCAGTAATCACTAAGAAGGTGGCTGATTGGTTGGTTTTCTGCTCCTCAAATATCGAG	459
Qy	4236	CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACT	4295
Db	460	CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACT	519
Qy	4296	GTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACG	4355
Db	520	GTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACAGCTGGTCTTTGGCATTGACG	579
Qy	4356	TGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCT	4415
Db	580	TGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTTGTACCTGCCTAGGTCTCTCCT	639
Qy	4416	ATGATGGCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCC	4475
Db	640	ATGATGGCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCCTGATAATTGTCC	699
Qy	4476	TGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGA	4535
Db	700	TGGTCATGATCGCAATAGAGGGCGGCTGTGCCCTGAGGAGGAAATCTGGGAGGAGCTGA	759
Qy	4536	GTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCAGGAAGCTGC	4595
Db	760	GTATGTTGGAGGTGTATGAGGGGAAGGAGGACAGTGTCTTCGCACATCCCAGGAAGCTGC	819
Qy	4596	TCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATC	4654
Db	820	TCATGCAAGATCTGGTGCAGGAAAACACCTGGAGTACCGGCAGGTGCCGGGCAGTGATC	879
Qy	4655	CCGCACGCTATGAGTTCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAG	4714
Db	880	CTGCATGCTACGAGTTCTGTGGGGTCCAAGGGCCCTCATTGAAACCAGCTATGTGAAAG	939
Qy	4715	TCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCTTTTTCTTCCCATCCCTGCGTG	4774
Db	940	TCCTGCACCATACTAAAGATCGGTGAAGAACCTCACATTTCTACCCACCCTGCATG	999
Qy	4775	AAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTG	4834
Db	1000	AACGGGCTTTGAGAGAGGGAGAAGAGTGAGTCTCAGCACAAAGTTGCAGCCAAGGCCAGTG	1059
Qy	4835	GGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCTCCAGCAGCTTCCCTGCCTCGT	4894
Db	1060	GGAGGGGGACTGGGCCAGTGCACCTTCCAGGGACCCATCCAGCAACTTCCACTGCCTCGA	1119
Qy	4895	GTGACATGAGGCCCATTCCTT--CACTCTGAAGAGAGCGGTGAGTGTTCTCAGTAGTAGGT	4952
Db	1120	GTGACATGAGGCCCATTCCTGCCTCTTTGAAGAGAGCAGTCAGCATTCCTTAGCAGTGAGT	1179
Qy	4953	TTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAAATTGTTCAAATG	5012
Db	1180	TTCTGTTCTGTTGGATGACTTTGAGATTTATCTTTGTTTCTGTTGGAAATTGTTCAAATG	1239

```

Qy      5013 TTTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTC 5072
      ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1240 TTCC-TTTTAACAAATGGTTGGATGAAC TTCAGCATCCAAGTTTATGAATGACAGTAGTC 1298

Qy      5073 ACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGA 5130
      ||||  |||  ||||  |||||  |||||  |||||  |||  |||||  |||||  |||||
Db      1299 ACACATAGTGCTGTTTATATAGTTTAGGGGTAAGAGTCCTGTTTTTTATTTCAGATTGGGA 1358

Qy      5131 AATCCATTCTATTTTGTGAATTG--GGATAATAACAGCAGTGGAATAAGTACTTAGAAAT 5188
      |||||  |||||  |||||  ||||  |||||  |||||  |||||  |||||  ||||  ||
Db      1359 AATCCATTCCATTTTGTGAGTTGTTCACATAATAACAGCAGTGGAATATGTATTTGCCTAT 1418

Qy      5189 GT----GAAAAATGAGCAGTAAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAG 5244
      |  |  |  |||  |||||  |||||  ||||  |  ||  ||||  |  ||  |||||
Db      1419 ATTGTGAACGAATTAGCAGTAAAAATACATGATACAAGGAAC-----TCAAAAGATAG 1470

Qy      5245 TCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATATGCATACCT 5304
      |  |||||  |||||  |||||  |||||  |||||  |||||  |||||  ||||  |||
Db      1471 TTAATTCTTGCCTTATACCTCAGTCTATTATGTAAAA--TTAAAAATATGTGTA----- 1522

Qy      5305 GGATTTTCCTTGGCTTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAGAATT 5359
      |  ||  |||||  |||||  |||||  |||||  |||||  |||||  ||  ||||
Db      1523 ----TGTTTTTGCTTCTTTGAGAATGCAAAAGAAATTAATCTAGGTAGGTAATT 1573

```

RESULT 13

```

US-11-266-748A-112460
; Sequence 112460, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 112460
; LENGTH: 1577
; TYPE: DNA
; ORGANISM: Homo Sapiens

```

US-11-266-748A-112460

Query Match 20.9%; Score 1188.2; DB 8; Length 1577;
Best Local Similarity 89.4%; Pred. No. 4.1e-299;
Matches 1390; Conservative 0; Mismatches 133; Indels 32; Gaps 9;

Qy	3816	GCCTGTGGGTCTTCATTGCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG	3875
Db	40	GCCTGTGGGTCTTCATTGCCAGCTCCTGCCCACACTCCTGCCTGTTGCCCTGACGAGAG	99
Qy	3876	TCATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCC	3935
Db	100	TCATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCC	159
Qy	3936	AACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCACCTCCTCCTCTCCTCTGG	3995
Db	160	AACAAGAGGCCCTGGGCCTGGTGTGTGTGCAGGCTGCCGCCTCCTCCTCTCCTCTGG	219
Qy	3996	TCCTGGGCACCCTGGAGGAGGTGCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC	4055
Db	220	TCCTGGGCACCCTGGAGGAGGTGCCACTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC	279
Qy	4056	AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGG	4115
Db	280	AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGG	339
Qy	4116	GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTC	4175
Db	340	GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTC	399
Qy	4176	GAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAG	4235
Db	400	GAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAG	459
Qy	4236	CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACT	4295
Db	460	CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTATCAAAAATTACAAGCACT	519
Qy	4296	GTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACG	4355
Db	520	GTTTTCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGACGCTGGTCTTTGGCATTGACG	579
Qy	4356	TGAAGGAAGCAGACCCACCGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCT	4415
Db	580	TGAAGGAAGCAGACCCACCGCCACTCCTATGTCCTTGTCACCTGCCTAGGTCTCTCCT	639
Qy	4416	ATGATGGCCTGCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCC	4475
Db	640	ATGATGGCCTGCTGGGTGATAATCAGATCATGCCAAGACAGGCTTCCTGATAATTGTCC	699
Qy	4476	TGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGA	4535
Db	700	TGGTCATGATCGCAATAGAGGGCGGCTGTGCCCTGAGGAGGAAATCTGGGAGGAGCTGA	759
Qy	4536	GTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGC	4595
Db	760	GTATGTTGGAGGTGTATGAGGGGAAGGAGGACAGTGTCTTCGCACATCCAGGAAGCTGC	819
Qy	4596	TCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATC	4654
Db	820	TCATGCAAGATCTGGTGCAGGAAAAGTACCTGGAGTACCGGCAGGTGCCGGGACAGTGATC	879

Qy	4655	CCGCACGCTATGAGTTTCCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAAG	4714
Db	880	CTGCATGCTACGAGTTTCCTGTGGGGTCCAAGGGCCCTCATTGAAACCAGCTATGTGAAAAG	939
Qy	4715	TCCTTGAGTATGTGATCAAGGTCAGTGCAAGAGTTTCGCTTTTCTTCCCATCCCTGCGTG	4774
Db	940	TCCTGCACCATACTACTAAAGATCGGTGAAGAACCTCACATTTCTTACCCACCCCTGCATG	999
Qy	4775	AAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTG	4834
Db	1000	AACGGGCTTTGAGAGAGGGAGAAGAGTGAGTCTCAGCACAAAGTTGCAGCCAAGGCCAGTG	1059
Qy	4835	GGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCTGCCTCGT	4894
Db	1060	GGAGGGGGACTGGGCCAGTGCACCTTCCAGGGACCCATCCAGCAACTTCCACTGCCTCGA	1119
Qy	4895	GTGACATGAGGCCCATTTCTT--CACTCTGAAGAGAGCGGTCAGTGTTCTCAGTAGTAGGT	4952
Db	1120	GTGACATGAGGCCCATTTCTTGCCTCTTTGAAGAGAGCAGTCAGCATTCTTAGCAGTGAGT	1179
Qy	4953	TTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAATTGTTCAAATG	5012
Db	1180	TTCTGTTCTGTTGGATGACTTTGAGATTTATCTTTGTTTCTGTTGGAATTGTTCAAATG	1239
Qy	5013	TTTTTTTTTAAAGGATGGTTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTC	5072
Db	1240	TTCC-TTTTAACAAATGGTTGGATGAAC TTCAGCATCCAAGTTTATGAATGACAGTAGTC	1298
Qy	5073	ACAC--AGTTCGTGTATATAGTTTAAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGA	5130
Db	1299	ACACATAGTGCTGTTTATATAGTTTAGGGGTAAGAGTCCTGTTTTTTATTTCAGATTGGGA	1358
Qy	5131	AATCCATTCTATTTTGTGAATTG--GGATAATAACAGCAGTGGAATAAGTACTTAGAAAT	5188
Db	1359	AATCCATTCCATTTTGTGAGTTGTACATAATAACAGCAGTGGAATATGTATTTGCCTAT	1418
Qy	5189	GT----GAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAG	5244
Db	1419	ATTGTGAACGAATTAGCAGTAAAATACATGATACAAGGAAC-----TCAAAAGATAG	1470
Qy	5245	TCAATTCTTGCCCTTATACCTCAGTCTATTCTGTAAAATTTTTAAAGATATATGCATACCT	5304
Db	1471	TTAATTCTTGCCCTTATACCTCAGTCTATTATGTAAAA--TTAAAAATATGTGTA-----	1522
Qy	5305	GGATTTCCTTGCCCTCTTTGAGAATGTAAGAGAAATTAATCTGAATAAAGAATT	5359
Db	1523	----TGTTTTTGCTTCTTTGAGAATGCAAAAGAAATTAATCTAGGTAGGTAATT	1573

```

; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 140662
; LENGTH: 1577
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-140662

```

```

Query Match          20.9%; Score 1188.2; DB 8; Length 1577;
Best Local Similarity 89.4%; Pred. No. 4.1e-299;
Matches 1390; Conservative 0; Mismatches 133; Indels 32; Gaps 9;

```

```

Qy      3816 GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1538 GCCTGTGGGTCTTCATTGCCCAGCTCCTGCCCACACTCCTGCCTGTTGCCCTGACGAGAG 1479

Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1478 TCATCATGTCTCTTGAGCAGAGGAGTCTGCAAGCCTGAGGAAGCCCTTGAGGCCC 1419

Qy      3936 AACAAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCACCTCCTCCTCTCTCTG 3995
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1418 AACAAAGAGGCCCTGGGCCTGGTGTGTGTGTCAGGCTGCCGCCTCCTCCTCTCTCTG 1359

Qy      3996 TCCTGGGACCCCTGGAGGAGGTGCCCACCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC 4055
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1358 TCCTGGGACCCCTGGAGGAGGTGCCCACCTGCTGGGTCAACAGATCCTCCCCAGAGTCCTC 1299

Qy      4056 AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCGACAGAGGCAACCCAGTGAGG 4115
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1298 AGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTCAACAGAGGCAACCCAGTGAGG 1239

Qy      4116 GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCC 4175
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1238 GTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTTGTATCCTGGAGTCCTTGTTCC 1179

Qy      4176 GAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAG 4235
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1178 GAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTTTTCTGCTCCTCAAATATCGAG 1119

Qy      4236 CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACT 4295
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1118 CCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTGTTCATCAAAAATTACAAGCACT 1059

```

Qy	4296	GTTTTTCCTGAGATCTTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACG	4355
Db	1058		
Qy	4356	GTTTTTCCTGAGATCTTTCGGCAAAGCCTCTGAGTCCTTGCAGCTGGTCTTTGGCATTGACG	999
Qy	4356	TGAAGGAAGCAGACCCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCAGGTCTCTCCT	4415
Db	998		
Qy	4356	TGAAGGAAGCAGACCCCCACCGGCCACTCCTATGTCCTTGTCACCTGCCAGGTCTCTCCT	939
Qy	4416	ATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCTTGATAATTGTCC	4475
Db	938		
Qy	4416	ATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGACAGGCTTCTTGATAATTGTCC	879
Qy	4476	TGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGGAGGAAATCTGGGAGGAGCTGA	4535
Db	878		
Qy	4476	TGGTCATGATCGCAATAGAGGGCGGCTGTGCCCTGAGGAGGAAATCTGGGAGGAGCTGA	819
Qy	4536	GTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCTATGGGGAGCCCAGGAAGCTGC	4595
Db	818		
Qy	4536	GTATGTTGGAGGTGTATGAGGGGAAGGAGGACAGTGTCTTCGCACATCCAGGAAGCTGC	759
Qy	4596	TCACCCAAGATTTGGTGCAGGAAAAGTACCTGGAGTA-CGGCAGGTGCCGGACAGTGATC	4654
Db	758		
Qy	4596	TCATGCAAGATCTGGTGCAGGAAAACACCTGGAGTACCGGCAGGTGCCGGGCAGTGATC	699
Qy	4655	CCGCACGCTATGAGTTTCTGTGGGGTCCAAGGGCCCTCGCTGAAACCAGCTATGTGAAAG	4714
Db	698		
Qy	4655	CTGCATGCTACGAGTTTCTGTGGGGTCCAAGGGCCCTCATTGAAACCAGCTATGTGAAAG	639
Qy	4715	TCCTTGAGTATGTGATCAAGGTCAGTGCAGAGTTTCGCTTTTTTCTTCCCATCCCTGCGTG	4774
Db	638		
Qy	4715	TCCTGCACCATACACTAAAGATCGGTGAAGAACCTCACATTTCTACCCACCCCTGCATG	579
Qy	4775	AAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCATGAGTTGCAGCCAAGGCCAGTG	4834
Db	578		
Qy	4775	AACGGGCTTTGAGAGAGGGAGAAGAGTGAAGTCTCAGCACAAAGTTGCAGCCAAGGCCAGTG	519
Qy	4835	GGAGGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTCCAGCAGCTTCCCCTGCCTCGT	4894
Db	518		
Qy	4835	GGAGGGGGACTGGGCCAGTGCACCTTCCAGGGACCCATCCAGCAACTTCCACTGCCTCGA	459
Qy	4895	GTGACATGAGGCCCATTCTT--CACTCTGAAGAGAGCGGTGAGTGTCTCAGTAGTAGGT	4952
Db	458		
Qy	4895	GTGACATGAGGCCCATTCTTGCCTCTTTGAAGAGAGCAGTCAGCATTCCTTAGCAGTGAGT	399
Qy	4953	TTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTCTCTTTTGGAAATTGTTCAAATG	5012
Db	398		
Qy	4953	TTCTGTTCTGTTGGATGACTTTGAGATTTATCTTTGTTTCTGTTGGAATTGTTCAAATG	339
Qy	5013	TTTTTTTTTAAGGGATGGTTGAATGAAC TTCAGCATCCAAGTTTATGAATGACAGCAGTC	5072
Db	338		
Qy	5013	TTCC-TTTTAACAAATGGTTGGATGAAC TTCAGCATCCAAGTTTATGAATGACAGTAGTC	280
Qy	5073	ACAC--AGTTCGTGTATATAGTTTAAGGGTAAGAGTCTTGTGTTTTATTTCAGATTGGGA	5130
Db	279		
Qy	5073	ACACATAGTGCTGTTTATATAGTTTAGGGTAAGAGTCCTGTTTTTTATTTCAGATTGGGA	220
Qy	5131	AATCCATTCTATTTTGTGAATTG--GGATAATAACAGCAGTGGAATAAGTACTTAGAAAT	5188
Db	219		
Qy	5131	AATCCATTCCATTTTGTGAGTTGTCACATAATAACAGCAGTGGAATATGTATTTCCTAT	160

```

Qy      5189 GT----GAAAAATGAGCAGTAAAATAGATGAGATAAAGAACTAAAGAAATTAAGAGATAG 5244
          |      |   ||| ||||| ||||| ||||| | || |||||
Db      159 ATTGTGAACGAATTAGCAGTAAAATACATGATACAAGGAAC-----TCAAAAGATAG 108

Qy      5245 TCAATTCTTGCCTTATACCTCAGTCTATTCTGTAAAATTTTAAAGATATATGCATACCT 5304
          | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      107 TTAATTCTTGCCTTATACCTCAGTCTATTATGTAAAA--TTAAAAATATGTGTA----- 56

Qy      5305 GGATTTCTTGGCTTCTTTGAGAATGTAAGAGAAATTAAATCTGAATAAAGAATT 5359
          |   || ||||| ||||| ||||| ||||| ||||| |||||
Db      55 ----TGTTTTGCTTCTTTGAGAATGCAAAAGAAATTAAATCTAGGTAGGTAATT 5

```

RESULT 15

US-11-253-240-11

; Sequence 11, Application US/11253240

; Publication No. US20060127356A1

; GENERAL INFORMATION:

; APPLICANT: Gaugler, Batrice; Van den Eynde, BenoEt;
 ; van der Bruggen, Pierre; Boon-Falleur, Thierry
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
 ; Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/11/253,240
 ; FILING DATE: 17-Oct-2005
 ; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/579,543
 ; FILING DATE: 26-May-2000
 ; APPLICATION NUMBER: 09/583,850
 ; FILING DATE:
 ; APPLICATION NUMBER: PCT/US92/04354
 ; FILING DATE: 22-MAY-1992
 ; APPLICATION NUMBER: 07/807,043
 ; FILING DATE: 12-DECEMBER-1991
 ; APPLICATION NUMBER: 07/764,365
 ; FILING DATE: 23-SEPTEMBER-1991
 ; APPLICATION NUMBER: 07/728,838
 ; FILING DATE: 9-JULY-1991
 ; APPLICATION NUMBER: 07/705,702
 ; FILING DATE: 23-MAY-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, Norman D.
 ; REGISTRATION NUMBER: 30,946
 ; REFERENCE/DOCKET NUMBER: LUD 5353

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 11:

```

; SEQUENCE CHARACTERISTICS:
;     LENGTH: 1640 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
;     NAME/KEY: cDNA MAGE-3
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-253-240-11

```

```

Query Match          17.4%; Score 988.8; DB 8; Length 1640;
Best Local Similarity 81.5%; Pred. No. 4.4e-247;
Matches 1253; Conservative 0; Mismatches 252; Indels 33; Gaps 8;

```

```

Qy      3816 GCCTGTGGGTCTTCATTGCCAGCTCCTGCCCACACTCCTGCCTGCTGCCCTGACGAGAG 3875
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      107 GCCAGTGGGTCTCCATTGCCAGCTCCTGCCCACACTCCCGCCTGTTGCCCTGACCAGAG 166

Qy      3876 TCATCATGTCTCTTGAGCAGAGGAGTCTGCACTGCAAGCCTGAGGAAGCCCTTGAGGCCC 3935
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      167 TCATCATGCCTCTTGAGCAGAGGAGTCAGCACTGCAAGCCTGAAGAAGGCCCTTGAGGCCC 226

Qy      3936 AACAAAGAGGCCCTGGGCCTGGTGTGTGTGCAAGGCT-----GCCA 3974
        | ||||| ||||| ||| ||||| ||||| |||||
Db      227 GAGGAGAGGCCCTGGGCCTGGTGGGTGCGCAGGCTCCTGCTACTGAGGAGCAGGAGGCTG 286

Qy      3975 CCTCCTCCTCCTCTCCTCTGGTCCCTGGGCACCCTGGAGGAGGTGCCCACTGCTGGGTCAA 4034
        ||||| ||||| ||| |||| ||| ||||| ||||| ||||| |||||
Db      287 CCTCCTCCTCTTCTACTCTAGTTGAAGTCACCCTGGGGGAGGTGCCTGCTGCCGAGTCAC 346

Qy      4035 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCGCCTTTCCCACTACCATCAACTTCACTC 4094
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      347 CAGATCCTCCCCAGAGTCCTCAGGGAGCCTCCAGCCTCCCCACTACCATGAAGTACCCCTC 406

Qy      4095 GACAGAGGCAACCCAGTGAGGGTTCCAGCAGCCGTGAAGAGGAGGGGCCAAGCACCTCTT 4154
        ||| ||| || ||||| ||||| || ||||| ||||| |||||
Db      407 TCTGGAGCCAATCCTATGAGGACTCCAGCAACCAAGAAGAGGAGGGGCCAAGCACCTTCC 466

Qy      4155 GTATCCTGGAGTCCTTGTTCGAGCAGTAATCACTAAGAAGGTGGCTGATTTGGTTGGTT 4214
        | ||||| ||||| ||||| ||||| ||| || ||||| ||||| |||||
Db      467 CTGACCTGGAGTCCGAGTTCCAAGCAGCACTCAGTAGGAAGGTGGCCGAGTTGGTTTATT 526

Qy      4215 TTCTGCTCCTCAAATATCGAGCCAGGGAGCCAGTCACAAAGGCAGAAATGCTGGAGAGTG 4274
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      527 TTCTGCTCCTCAAGTATCGAGCCAGGGAGCCGGTCACAAAGGCAGAAATGCTGGGGAGTG 586

Qy      4275 TCATCAAAAATTACAAGCACTGTTTTCCTGAGATCTTCGGCAAAGCCTCTGAGTCCTTGC 4334
        || || ||||| || ||| ||||| ||||| ||||| ||||| |||||
Db      587 TCGTCGGAATTGGCAGTATTTCTTTCTGTGATCTTCAGCAAAGCTTCCAGTTCTCTTGC 646

Qy      4335 AGCTGGTCTTTGGCATTGACGTGAAGGAAGCAGACCCACCGGCCACTCCTATGTCTCTTG 4394
        ||||| ||||| || ||| ||||| ||||| ||||| ||||| |||||
Db      647 AGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCATCGGCCACTTGTACATCTTTG 706

Qy      4395 TCACCTGCCTAGGTCTCTCCTATGATGGCCTGCTGGGTGATAATCAGATCATGCCCAAGA 4454
        ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Db      707 CCACCTGCCTGGGCCTCTCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCCAAGG 766

Qy      4455 CAGGCTTCCTGATAATTGTCCTGGTCATGATTGCAATGGAGGGCGGCCATGCTCCTGAGG 4514
        ||||| ||||| ||||| ||||| ||| || ||||| ||||| |||||

```

Db		767 CAGGCCCTCCTGATAATCGTCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGG	826
Qy	4515 AGGAAATCTGGGAGGAGCTGAGTGTGATGGAGGTGTATGATGGGAGGGAGCACAGTGCCT	4574	
Db	827 AGAAAATCTGGGAGGAGCTGAGTGTGTTAGAGGTGTTTTGAGGGGAGGAAGACAGTATGT	886	
Qy	4575 ATGGGGAGCCCAGGAAGCTGCTCACCCAAGATTGGTGCAGGAAAAGTACCTGGAGTA-C	4633	
Db	887 TGGGGGATCCCCAAGAAGCTGCTCACCCAACATTTCTGTCAGGAAAACACCTGGAGTACC	946	
Qy	4634 GGCAGGTGCCGGACAGTGATCCCGCACGCTATGAGTTCCTGTGGGGTCCAAGGGCCCTCG	4693	
Db	947 GGCAGGTCCCCGGCAGTGATCCTGCATGTTATGAATTCCTGTGGGGTCCAAGGGCCCTCG	1006	
Qy	4694 CTGAAACCAGCTATGTGAAAGTCC TTGAGTATGTGATCAAGGTCAGTGCAAGAGTTCGCT	4753	
Db	1007 TTGAAACCAGCTATGTGAAAGTCC TGACCATATGGTAAAGATCAGTGGAGGACCTCACA	1066	
Qy	4754 TTTCTTCCCATCCCTGCGTGAAGCAGCTTTGAGAGAGGAGGAAGAGGGAGTCTGAGCAT	4813	
Db	1067 TTTCTACCCACCCCTGCATGAGTGGGTTT TGAGAGAGGGGGAAGAGTGAGTCTGAGCAC	1126	
Qy	4814 GAGTTGCAGCCAAGGCCAGTGGGAGGGGACTGGGCCAGTGCACCTTCCAGGGCCGCGTC	4873	
Db	1127 GAGTTGCAGCCAGGGCCAGTGGGAGGGGTCTGGGCCAGTGCACCTTCCGGGGCCGCATC	1186	
Qy	4874 CAGCAGCTTCCCCTGCCTCGTGTGACATGAGGCCCATTCTTCACTC--TGAAGAGAGCGG	4931	
Db	1187 CCTTAGTTTCCACTGCCTCCTGTGACGTGAGGCCCATTCTTCACTCTTTGAAGCGAGCAG	1246	
Qy	4932 TCAGTGTCTCAGTAGTAGGTTTCTGTTCTATTGGGTGACTTGGAGATTTATCTTTGTTC	4991	
Db	1247 TCAGCATCTTAGTAGTGGGTTTCTGTTCTGTTGGATGACTTTGAGATTATTCTTTGTTT	1306	
Qy	4992 TCTTTTGGAATTGTTCAAATGTTTTTTTTTTAAGGGATGGTTGAATGAATTCAGCATCCA	5051	
Db	1307 CCTGTTGGAGTTGTTCAAATG-TTCCTTTAACGGATGGTTGAATGAGCGTCAGCATCCA	1365	
Qy	5052 AGTTTATGAATGACAGCAGTCACAC--AGTTCTGTGTATATAGTTTAAGGGTAAGAGTCT	5109	
Db	1366 GGTTTATGAATGACAGTAGTCACACATAGTGCTGTTTATATAGTTTAGGAGTAAGAGTCT	1425	
Qy	5110 TGTGTTTTATTTCAGATTGGGAAATCCATTCTATTTTGTGAATTGGG--ATAATAACAGCA	5167	
Db	1426 TGTTTTTTACTCAAATTGGGAAATCCATTCCATTTTGTGAATTGTGACATAATAATAGCA	1485	
Qy	5168 GTGGAATAAGTACTT-AGAAATGTGAAAAATGAGCAGTAAAATAGATGAGATAAAGA AACT	5226	
Db	1486 GTGGTAAAAGTATTTGCTTAAAATGTGAGCGAATTAGCAATAACATACATGAGATA AACT	1545	
Qy	5227 AAAGAAATTAAGAGATAGTCAATTCTTGCTTATACCTCAGTCTATTCTGTAAAAATTTT	5286	
Db	1546 CAAGAAATCAAAGATAGTTGATTCTTGCTTGTACCTCAATCTATTCTGTAAAA--TT	1602	
Qy	5287 AAAGATATATGCATACCTGGATTTCCTTGCTTCTTTG	5324	
Db	1603 AAACAAATATGCAAACAGGATTTTCCTTGACTTCTTTG	1640	

